

FORM PTO-1390 (Modified)
(REV 11-2000)

U.S. DEPARTMENT OF COMMERCE PATENT AND TRADEMARK OFFICE

ATTORNEY'S DOCKET NUMBER

**TRANSMITTAL LETTER TO THE UNITED STATES
DESIGNATED/ELECTED OFFICE (DO/EO/US)
CONCERNING A FILING UNDER 35 U.S.C. 371**

P23,495 USA

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR 1.5)

097807660

INTERNATIONAL APPLICATION NO.

PCT/US99/23641

INTERNATIONAL FILING DATE

13 October 1999 (13.10.99)

PRIORITY DATE CLAIMED

16 October 1998 (16.10.98)

TITLE OF INVENTION

METHODS OF INHIBITING PLATELET ACTIVATION AND RECRUITMENT

APPLICANT(S) FOR DO/EO/US

Charles R. MALISZEWSKI, Richard B. GAYLE III and Aaron J. MARCUS

Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f)). The submission must include items (5), (6), (9) and (24) indicated below.
4. ☒ The US has been elected by the expiration of 19 months from the priority date (Article 31).
5. ☒ A copy of the International Application as filed (35 U.S.C. 371 (c) (2))
 - a. ☐ is attached hereto (required only if not communicated by the International Bureau).
 - b. ☐ has been communicated by the International Bureau.
 - c. ☒ is not required, as the application was filed in the United States Receiving Office (RO/US).
6. ☐ An English language translation of the International Application as filed (35 U.S.C. 371(c)(2)).
 - a. ☐ is attached hereto.
 - b. ☐ has been previously submitted under 35 U.S.C. 154(d)(4).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371 (c)(3))
 - a. ☐ are attached hereto (required only if not communicated by the International Bureau).
 - b. ☐ have been communicated by the International Bureau.
 - c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
 - d. ☒ have not been made and will not be made.
8. ☐ An English language translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371 (c)(4)). (**unexecuted**)
10. ☐ An English language translation of the annexes of the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371 (c)(5)).
11. ☒ A copy of the International Preliminary Examination Report (PCT/IPEA/409), mailed on 02 March 2001 (02.03 01)
12. ☒ A copy of the International Search Report (PCT/ISA/210), mailed on 17 May 2000 (17.05.00)

Items 13 to 20 below concern document(s) or information included:

13. ☐ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
14. ☐ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
15. ☒ A **FIRST** preliminary amendment.
16. ☐ A **SECOND** or **SUBSEQUENT** preliminary amendment
17. ☐ A substitute specification.
18. ☐ A change of power of attorney and/or address letter.
19. ☒ A computer-readable form of the sequence listing in accordance with PCT Rule 13ter.2 and 35 U.S.C. 1.821 - 1.825.
20. ☐ A second copy of the published international application under 35 U.S.C. 154(d)(4).
21. ☐ A second copy of the English language translation of the international application under 35 U.S.C. 154(d)(4).
22. ☒ Certificate of Mailing by Express Mail, dated 16 April 2001 (16.04.01)
23. ☒ Other items or information:
 postcard;
 copy of Written Opinion, mailed on 18 August 2000 (18.08.00); and
 copy of Reply Under PCT Article 34 Sec. (2)(d) to Written Opinion Dated August 18, 2000, mailed on 13 December 2000 (13.12.00).

U.S. APPLICATION NO. (IF KNOWN, SEE 37 CFR 1.53) **09/807660** INTERNATIONAL APPLICATION NO. **PCT/US99/23641** ATTORNEY'S DOCKET NUMBER **P23,495 USA**

24. The following fees are submitted:.				CALCULATIONS PTO USE ONLY	
BASIC NATIONAL FEE (37 CFR 1.492 (a) (1) - (5)) :					
<input type="checkbox"/> Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO and International Search Report not prepared by the EPO or JPO \$1000.00					
<input checked="" type="checkbox"/> International preliminary examination fee (37 CFR 1.482) not paid to USPTO but International Search Report prepared by the EPO or JPO \$860.00					
<input type="checkbox"/> International preliminary examination fee (37 CFR 1.482) not paid to USPTO but international search fee (37 CFR 1.445(a)(2)) paid to USPTO \$710.00					
<input type="checkbox"/> International preliminary examination fee (37 CFR 1.482) paid to USPTO but all claims did not satisfy provisions of PCT Article 33(1)-(4) \$690.00					
<input type="checkbox"/> International preliminary examination fee (37 CFR 1.482) paid to USPTO and all claims satisfied provisions of PCT Article 33(1)-(4) \$100.00					
ENTER APPROPRIATE BASIC FEE AMOUNT =				\$860.00	
Surcharge of \$130.00 for furnishing the oath or declaration later than <input type="checkbox"/> 20 <input checked="" type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492 (e)).				\$130.00	
CLAIMS	NUMBER FILED	NUMBER EXTRA	RATE		
Total claims	29 - 20 =	9	x \$18.00	\$162.00	
Independent claims	3 - 3 =	0	x \$80.00	\$0.00	
Multiple Dependent Claims (check if applicable). <input type="checkbox"/>				\$0.00	
TOTAL OF ABOVE CALCULATIONS =				\$1,152.00	
Applicant claims small entity status. (See 37 CFR 1.27). The fees indicated above are reduced by 1/2.				\$0.00	
SUBTOTAL =				\$1,152.00	
Processing fee of \$130.00 for furnishing the English translation later than <input type="checkbox"/> 20 <input type="checkbox"/> 30 months from the earliest claimed priority date (37 CFR 1.492 (f)).				\$0.00	
TOTAL NATIONAL FEE =				\$1,152.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31) (check if applicable). <input type="checkbox"/>				\$0.00	
TOTAL FEES ENCLOSED =				\$1,152.00	
				Amount to be:	\$
				refunded	\$
				charged	\$

- a. ☒ A check in the amount of **\$1,152.00** to cover the above fees is enclosed.
- b. ☐ Please charge my Deposit Account No. _____ in the amount of _____ to cover the above fees. A duplicate copy of this sheet is enclosed.
- c. ☒ The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. **19-5425** A duplicate copy of this sheet is enclosed.
- d. ☐ Fees are to be charged to a credit card. **WARNING:** Information on this form may become public. **Credit card information should not be included on this form.** Provide credit card information and authorization on PTO-2038.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

Patrick J. Kelly, Ph.D., Esquire
SYNNESTVEDT & LECHNER LLP
2600 Aramark Tower
1101 Market Street
Philadelphia, Pennsylvania 19107-2950
United States of America
Telephone: (215) 923-4466
Facsimile: (215) 923-2189
E-mail: pkelly@synnlechn.com


SIGNATURE

Patrick J. Kelly
NAME

NAME

34,638
REGISTRATION NUMBER

REGISTRATION NUMBER

16 April 2001 (16.04.01)
DATE

DATE

LAW OFFICES OF
SYNNESTVEDT & LECHNER LLP
2600 ARAMARK TOWER
1101 MARKET STREET
PHILADELPHIA, PA 19107-2950
TELEPHONE (215) 923-4466
FACSIMILE (215) 923-2189
E-MAIL synnlech@synnlech.com
www.synnlech.com

April 16, 2001

IN THE UNITED STATES RECEIVING OFFICE
AS THE DO/EO OF THE PATENT COOPERATION TREATY

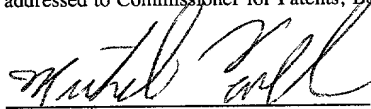
Re: Charles R. Maliszewski, Richard B. Gayle III
and Aaron J. Marcus
U.S. National Phase Application
Based on Intl. Application No. PCT/US99/23641
Filed October 13, 1999

METHODS OF INHIBITING
PLATELET ACTIVATION AND RECRUITMENT

Attorney Docket No. 23,495 USA

CERTIFICATE OF EXPRESS MAILING

I hereby certify that this correspondence is being deposited with the U.S. Postal Service as Express Mail Post Office to Addressee, Mailing Label No. EL598707094US, in an envelope addressed to Commissioner for Patents, Box Patent Application, Washington, DC 20231 on April 16, 2001.


Michael B. Lavelle

Commissioner for Patents
Box Patent Application
Washington, DC 20231

PRELIMINARY AMENDMENT

Sir:

Before commencing examination of the above-identified application, please amend the application as follows.

In the Specification

April 16, 2001

Please replace the paragraph beginning at page 2, line 1, with the following rewritten paragraph:

--Immunoprecipitation of HUVEC detergent lysates with anti-CD39 mAb resulted in complete capture of cell-associated ADPase activity, suggesting that CD39 is the only ecto-ADPase on endothelial cells (Marcus et al., *J. Clin. Invest.* 99:1351, 1997). In the same study, COS cell transfectants expressing recombinant CD39 at the cell surface totally inhibited ADP-induced platelet aggregation. Thus, CD39 plays a prominent role in thromboregulation (*see also*, Gayle et al., *J. Clin. Invest.*, 101:1851, 1998; WO96/30532).

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In the Claims

Cancel Claims 8 through 18.

Add new Claims 20 to 41.

--20. A method according to Claim 1 wherein the soluble CD39 polypeptide has been produced by culturing a recombinant cell that encodes the soluble CD39 polypeptide under conditions permitting expression of the CD39 polypeptide, and recovering the expressed CD39 polypeptide.

21. A method according to Claim 5 wherein the soluble CD39 polypeptide has been produced by culturing a recombinant cell that encodes the soluble CD39 polypeptide under conditions permitting expression of the CD39 polypeptide, and recovering the expressed CD39 polypeptide.

22. The method of claim 20 wherein the recombinant cell comprises a nucleic acid having a sequence selected from the group consisting of:

(a) SEQ ID NO:5; and

(b) DNA sequences which, due to degeneracy of the genetic code, encode the polypeptide encoded by SEQ ID NO:5.

April 16, 2001

23. The method of claim 21 wherein the recombinant cell comprises a nucleic acid having a sequence selected from the group consisting of:

- (a) SEQ ID NO:5; and
- (b) DNA sequences which, due to degeneracy of the genetic code, encode the polypeptide encoded by SEQ ID NO:5.

24. The method of claim 20 wherein the recombinant cell comprises a nucleic acid having a sequence selected from the group consisting of:

- (a) SEQ ID NO:7; and
- (b) DNA sequences which, due to degeneracy of the genetic code, encode the polypeptide encoded by SEQ ID NO:7.

25. The method of claim 21 wherein the recombinant cell comprises a nucleic acid having a sequence selected from the group consisting of:

- (a) SEQ ID NO:7; and
- (b) DNA sequences which, due to degeneracy of the genetic code, encode the polypeptide encoded by SEQ ID NO:7.

26. The method of Claim 1 wherein the soluble CD39 polypeptide is administered in a composition comprising a pharmaceutically acceptable carrier.

27. The method of Claim 5 wherein the soluble CD39 polypeptide is administered in a composition comprising a pharmaceutically acceptable carrier.

28. The method of Claim 1 wherein the soluble CD39 polypeptide is administered in combination with at least one other antithrombotic or antiplatelet composition.

29. The method of Claim 5 wherein the soluble CD39 polypeptide is administered in combination with at least one other antithrombotic or antiplatelet composition.

April 16, 2001

30. The method of claim 1 wherein the soluble CD39 polypeptide is administered in combination with aspirin.

31. The method of claim 5 wherein the soluble CD39 polypeptide is administered in combination with aspirin.

32. The method of Claim 1 wherein the soluble CD39 polypeptide is administered parenterally.

33. The method of Claim 5 wherein the soluble CD39 polypeptide is administered parenterally.

34. The method of claim 32 wherein the soluble CD39 polypeptide is administered intravenously.

35. The method of claim 33 wherein the soluble CD39 polypeptide is administered intravenously.

36. The method of Claim 1 wherein the mammal is suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, myocardial infarction, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, a platelet-associated ischemic disorder including lung ischemia, coronary ischemia, and cerebral ischemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis and coagulopathy associated with exposure to a foreign or injured tissue surface, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischemic attack (TIAs), or another related condition where vascular occlusion is the common underlying feature.

37. The method of Claim 5 wherein the mammal is suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, myocardial

April 16, 2001

infarction, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, a platelet-associated ischemic disorder including lung ischemia, coronary ischemia, and cerebral ischemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis and coagulopathy associated with exposure to a foreign or injured tissue surface, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischemic attack (TIAs), or another related condition where vascular occlusion is the common underlying feature.

38. The method of Claim 1 wherein the soluble CD39 is administered to prevent thrombus formation or reformation, occlusion, reocclusion, stenosis, or restenosis of blood vessels, or stroke.

39. The method of Claim 5 wherein the soluble CD39 is administered to prevent thrombus formation or reformation, occlusion, reocclusion, stenosis, or restenosis of blood vessels, or stroke.

40. The method of Claim 1 wherein the soluble CD39 is administered in conjunction with angioplasty, carotid endarterectomy, anastomosis of vascular graft, atherectomy, stent placement, placement of a chronic cardiovascular device such as an in-dwelling catheter or prosthetic valve or vessel, or bypass surgery.

41. The method of Claim 5 wherein the soluble CD39 is administered in conjunction with angioplasty, carotid endarterectomy, anastomosis of vascular graft, atherectomy, stent placement, placement of a chronic cardiovascular device such as an in-dwelling catheter or prosthetic valve or vessel, or bypass surgery.--

REMARKS

Claims 8 to 18 have been canceled, and presented as new Claims 20 to 41 to eliminate the multiple dependencies. Claims 1 to 7, and 19 to 41 are presented for examination.

April 16, 2001

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached page is captioned "Version with Markings to Show Changes Made".

Respectfully submitted,



Patrick J. Kelly, Ph.D., Esq.
Registration No. 34,638

SYNNESTVEDT & LECHNER LLP
Suite 2600 Aramark Tower
1101 Market Street
Philadelphia, PA 19107
(215) 923-4466

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1101 Market Street
Philadelphia, PA 19107
(215) 923-4466

April 16, 2001

VERSION WITH MARKINGS TO SHOW CHANGES MADE

In the Specification

The paragraph beginning at page 2, line 1, has been amended as follows:

Immunoprecipitation of HUVEC detergent lysates with anti-CD39 mAb resulted in complete capture of cell-associated ADPase activity, suggesting that CD39 is the only ecto-ADPase on endothelial cells (Marcus et al., *J. Clin. Invest.* 99:1351, 1997). In the same study, COS cell transfectants expressing recombinant CD39 at the cell surface totally inhibited ADP-induced platelet aggregation. Thus, CD39 plays a prominent role in thromboregulation (*see also*, Gayle et al., *J. Clin. Invest.*, 101:1851, 1998; WO96/30532).

Claims 8 through 18 have been canceled.

New Claims 20 to 41 have been added.

--20. A method according to [one of claims 1-7] Claim 1 wherein the soluble CD39 polypeptide has been produced by culturing a recombinant cell that encodes the soluble CD39 polypeptide under conditions permitting expression of the CD39 polypeptide, and recovering the expressed CD39 polypeptide.

21. A method according to [one of claims 1-7] Claim 5 wherein the soluble CD39 polypeptide has been produced by culturing a recombinant cell that encodes the soluble CD39 polypeptide under conditions permitting expression of the CD39 polypeptide, and recovering the expressed CD39 polypeptide.

22. The method of claim [8] 20 wherein the recombinant cell comprises a nucleic acid having a sequence selected from the group consisting of:

April 16, 2001

(a) SEQ ID NO:5; and

(b) DNA sequences which, due to degeneracy of the genetic code, encode the polypeptide encoded by SEQ ID NO:5.

23. The method of claim [8] 21 wherein the recombinant cell comprises a nucleic acid having a sequence selected from the group consisting of:

(a) SEQ ID NO:5; and

(b) DNA sequences which, due to degeneracy of the genetic code, encode the polypeptide encoded by SEQ ID NO:5.

24. The method of claim [8] 20 wherein the recombinant cell comprises a nucleic acid having a sequence selected from the group consisting of:

(a) SEQ ID NO:7; and

(b) DNA sequences which, due to degeneracy of the genetic code, encode the polypeptide encoded by SEQ ID NO:7.

25. The method of claim [8] 21 wherein the recombinant cell comprises a nucleic acid having a sequence selected from the group consisting of:

(a) SEQ ID NO:7; and

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26. The method of Claim 1 wherein the soluble CD39 polypeptide is administered in a composition comprising a pharmaceutically acceptable carrier.

27. The method of Claim 5 wherein the soluble CD39 polypeptide is administered in a composition comprising a pharmaceutically acceptable carrier.

28. The method of Claim 1 wherein the soluble CD39 polypeptide is administered in combination with at least one other antithrombotic or antiplatelet composition.

April 16, 2001

29. The method of Claim 5 wherein the soluble CD39 polypeptide is administered in combination with at least one other antithrombotic or antiplatelet composition.

30. The method of claim 1 wherein the soluble CD39 polypeptide is administered in combination with aspirin.

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32. The method of Claim 1 wherein the soluble CD39 polypeptide is administered parenterally.

33. The method of Claim 5 wherein the soluble CD39 polypeptide is administered parenterally.

34. The method of claim 32 wherein the soluble CD39 polypeptide is administered intravenously.

35. The method of claim 33 wherein the soluble CD39 polypeptide is administered intravenously.

36. The method of Claim 1 wherein the mammal is suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, myocardial infarction, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, a platelet-associated ischemic disorder including lung ischemia, coronary ischemia, and cerebral ischemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis and coagulopathy associated with exposure to a foreign or injured tissue surface, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischemic

April 16, 2001

attack (TIAs), or another related condition where vascular occlusion is the common underlying feature.

37. The method of Claim 5 wherein the mammal is suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, myocardial infarction, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, a platelet-associated ischemic disorder including lung ischemia, coronary ischemia, and cerebral ischemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis and coagulopathy associated with exposure to a foreign or injured tissue surface, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischemic attack (TIAs), or another related condition where vascular occlusion is the common underlying feature.

38. The method of Claim 1 wherein the soluble CD39 is administered to prevent thrombus formation or reformation, occlusion, reocclusion, stenosis, or restenosis of blood vessels, or stroke.

39. The method of Claim 5 wherein the soluble CD39 is administered to prevent thrombus formation or reformation, occlusion, reocclusion, stenosis, or restenosis of blood vessels, or stroke.

40. The method of Claim 1 wherein the soluble CD39 is administered in conjunction with angioplasty, carotid endarterectomy, anastomosis of vascular graft, atherectomy, stent placement, placement of a chronic cardiovascular device such as an in-dwelling catheter or prosthetic valve or vessel, or bypass surgery.

41. The method of Claim 5 wherein the soluble CD39 is administered in conjunction with angioplasty, carotid endarterectomy, anastomosis of vascular graft,

April 16, 2001

atherectomy, stent placement, placement of a chronic cardiovascular device such as an in-dwelling catheter or prosthetic valve or vessel, or bypass surgery.--

09/807660

JC05 Rec'd PCT/PTO 16 APR 2001

LAW OFFICES OF
SYNNESTVEDT & LECHNER LLP

2600 ARAMARK TOWER
1101 MARKET STREET
PHILADELPHIA, PA 19107-2950
TELEPHONE (215) 923-4466
FACSIMILE (215) 923-2189
E-MAIL synnlech@synnlech.com
www.synnlech.com

16 April 2001

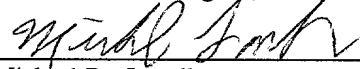
IN THE UNITED STATES RECEIVING OFFICE
OF THE PATENT COOPERATION TREATY

In Re: Application of Charles R. Maliszewski, et al.
Application No. Not Yet Assigned
Based on Int'l Appln. No. PCT/US99/23641
METHODS OF INHIBITING
PLATELET ACTIVATION AND RECRUITMENT

Attorney Docket No. P23,495 USA

CERTIFICATE OF EXPRESS MAILING

I hereby certify that this correspondence is being deposited with the U.S. Postal Service as Express Mail Post Office to Addressee, Mailing Label No. EL 598707094US, addressed to Commissioner for Patents, Box PCT, Attention: DO/EO/US, Washington, DC 20231 on 16 April 2001.



Michael B. Lavelle

Commissioner for Patents
Box PCT
Attention: DO/EO/US
Washington, DC 20231

SEQUENCE LISTING CERTIFICATION

Sir:

In accordance with the rules set forth for an Application Disclosure
Containing Nucleotide and/or Amino Acid Sequences, I hereby certify that the

Charles R. Maliszewski, et al.
Page 2

16 April 2001

content of the paper and computer-readable copies of the sequences contained in the above-identified application are the same.

Respectfully submitted,

SYNNESTVEDT & LECHNER LLP



Patrick J. Kelly, Ph.D., Esq.
Reg. No. 34,638

Suite 2600 Aramark Tower
1101 Market Street
Philadelphia, PA 19107
(215) 923-4466

M:\LWhite\Immunex-Cornell\23495 PCT\23495 USA sequence verification.wpd

2001 APR 16 PM 4:05

13 Rec'd PCT/PTO 03 SEP 2001

09/807660

LAW OFFICES OF
SYNNESTVEDT & LECHNER LLP

2600 ARAMARK TOWER
1101 MARKET STREET
PHILADELPHIA, PA 19107-2950
TELEPHONE (215) 923-4466
FACSIMILE (215) 923-2189
E-MAIL synnlech@synnlech.com
www.synnlech.com

September 4, 2001

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re\ Application of: Charles R. Maliszewski, Richard B. Gayle III
and Aaron J. Marcus
Application No.: 09/807,660
Filed: April 16, 2001

Examiner
Art Unit

METHODS OF INHIBITING PLATELET ACTIVATION AND RECRUITMENT

(Atty. Docket No. 23,495 USA)

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service as first-class mail, postage prepaid, in an envelope addressed to: Commissioner for Patents, BOX PCT, Washington, DC 20231 on September 4, 2001.


Lynn M. White

Commissioner for Patents
BOX PCT
Washington, DC 20231

TRANSMITTAL LETTER

Sir:

In response to the Notification to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid Sequence Disclosures (hereinafter "Notice") dated June 1, 2001, enclosed herewith are the following:

- (A) Computer-readable and paper copies of the Sequence Listing; and
- (B) Copy of Patent and Trademark Office document entitled "Notice to Comply with Requirements for Patent Applications Containing Nucleotide Sequence and/or Amino Acid sequence Disclosures".

September 4, 2001

Remarks

The Notice of June 1, 2001 refers to the requirement to provide a replacement Sequence Listing for amino acid and nucleotide sequences which appear in the above-identified application in computer-readable form. Computer-readable and paper copies of the Sequence Listing are provided herewith pursuant to 37 CFR §1.821.

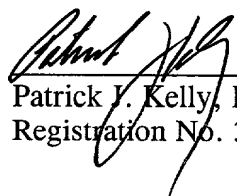
STATEMENT

In accordance with 37 CFR §1.821(g) relating to submissions containing Sequence Listings after the time of filing of the application, the undersigned hereby certifies that:

- (A) the contents of the computer-readable copy of the Sequence Listing submitted herewith and the paper copy of the Sequence Listing are the same;
- (B) all of the sequences are reflected in the application as filed; and
- (C) the present submission contains no new matter.

Any Patent Office fee associated with this matter should be charged to Deposit Account No. 19-5425. A duplicate of this transmittal letter is enclosed.

Respectfully submitted,



Patrick J. Kelly, Ph.D.
Registration No. 34,638

SYNNESTVEDT & LECHNER LLP
Suite 2600 Aramark Tower
1101 Market Street
Philadelphia, PA 19107

TITLEMETHODS OF INHIBITING PLATELET ACTIVATION AND RECRUITMENTREFERENCE TO RELATED APPLICATIONS

5 The present application is related to U.S. Provisional Application Serial Nos. 60/104,585, filed 16 October 1998, 60/107,466, filed 06 November 1998, and 60/149,010, filed 13 August 1999.

FIELD OF THE INVENTION

10 This invention relates to soluble CD39 compounds and compositions, the preparation thereof, and the use thereof to inhibit platelet activation and recruitment in a mammal.

BACKGROUND OF THE INVENTION

CD39 is a cell-surface antigen that was originally identified as a marker for mature B cells, but is also expressed on less mature B cells, Epstein-Barr Virus-transformed B cells, activated T cells, endothelial cells and some myeloid cell lines (Dörken et al., in *Leukocyte Typing IV*; W. Knapp, B. Dörken, and W.R. Gilks, Eds; Oxford University Press, New York, NY; pp. 89-90, 1989). Monoclonal antibodies against CD39 induce B cell homotypic adhesion, an activity that may be important in the regulation of immune function (Kansas and Tedder, *J. Immunol.* 147:4094-4102, 1991). Molecular cloning and characterization of CD39 indicated that it is unique cell surface molecule that contains two potential transmembrane regions and a hydrophobic segment within the putative extracellular domain (Maliszewski et al., *J. Immunol.* 153:3574, 1994). The amino acid sequence of CD39 was reported to exhibit some homology with a guanosine diphosphatase from yeast (Maliszewski et al., *supra*).

In 1996, an ATP diphosphohydrolase was cloned from potato tubers (Handa and Guidotti, *Biochem. Biophys. Res. Commun.* 218:916, 1996). The amino acid sequences of this and several other NTPases demonstrated a high degree of similarity, particularly within several small "apyrase conserved regions" (ACR). CD39 shares these conserved regions with soluble ATP-diphosphorylase from potato tubers, other apyrases and related enzymes. It was subsequently reported that native and recombinant full-length CD39 possess E-type ATP diphosphohydrolase (ATPDase) activity (Marcus et al., *J. Clin. Invest.* 99:1351, 1997); Kaczmarek et al., *J. Biol. Chem.* 271:33116, 1996); Wang and Guidotti, *J. Biol. Chem.* 271:9898, 1996). ATPDases degrade nucleoside tri- and/or diphosphates, but not monophosphates (Plesner, *Int. Rev. Cytol.* 158:141, 1995).

Vascular endothelial cells constitutively express a cell-surface ADPase (ecto-ATP diphosphohydrolase, apyrase, EC 3.6.1.5), one of at least 3 thromboregulatory systems which function in the maintenance of blood fluidity (Marcus and Safier, *FASEB J.* 7:516, 1983; Marcus et al., *J. Clin. Invest.* 88:1690, 1991). This ecto-ADPase, which belongs to the E-type ATPDase family, rapidly metabolizes ADP in the platelet releasate, terminating further platelet recruitment and aggregation.

ART 34 AMDT

23,495 PCT

Immunoprecipitation of HUVEC detergent lysates with anti-CD39 mAb resulted in complete capture of cell-associated ADPase activity, suggesting that CD39 is the only ecto-ADPase on endothelial cells (Marcus et al., *J. Clin. Invest.* 99:1351, 1997). In the same study, COS cell transfectants expressing recombinant CD39 at the cell surface totally inhibited ADP-induced platelet aggregation. Thus, CD39 plays a prominent role in thromboregulation (*see also*, Gayle et al., *J. Clin. Invest.*, 101:1851, 1998; WO96/30532).

Excessive platelet activation (i.e., stimulation by an agonist) and recruitment, leading to platelet aggregation and vessel occlusion at sites of vascular injury in the coronary, carotid, and peripheral arteries, presents a major therapeutic challenge in cardiovascular medicine. Excessive platelet activation and recruitment is a contributing factor in clinical disorders including stroke, unstable angina, myocardial infarction, and restenosis following percutaneous coronary intervention including angioplasty, atherectomy, stent placement, and bypass surgery.

Glycoprotein IIb/IIIa antagonists, such as the monoclonal antibody marketed as ReoPro® (Centocor Inc.), are presently under development for the inhibition of platelet aggregation in patients undergoing percutaneous coronary intervention, and in patients with acute coronary syndromes such as unstable angina and myocardial infarction. The activation of glycoprotein IIb/IIIa receptors, however, is a late event in the cascade that leads to platelet aggregation.

There is a great need to identify additional therapeutic strategies and compositions for the pharmacological neutralization of platelet reactivity (activation, recruitment, aggregation). In particular, there is a need to identify compounds and compositions which target early portions of coagulation pathways such as the ADP-dependent activation and recruitment of platelets. There is, in fact, an urgent need to identify new strategies and compositions for the treatment of stroke, which is the third leading cause of death in the United States. In the case of stroke, an advantageous therapeutic agent will reduce intravascular thrombus burden and accompanying neurological defects without increasing intracerebral hemorrhage.

SUMMARY OF THE INVENTION

Soluble forms of CD39 having apyrase activity constitute a novel approach to the prevention and/or treatment of disease. The present invention provides soluble CD39 polypeptides and nucleic acids, compositions comprising a pharmaceutically acceptable carrier and a soluble CD39 polypeptide, and methods of making and using soluble CD39 polypeptides having apyrase activity. The effectiveness of soluble CD39 polypeptides have been demonstrated in vitro, ex vivo, and in vivo.

The invention is directed to soluble CD39 polypeptides selected from the group consisting of: (a) polypeptides having an amino acid sequence as set forth in Figure 1 (SEQ ID NO:2) wherein the amino terminus is selected from the group consisting of amino acids 36-44, and the carboxy terminus is selected from the group consisting of amino acids 471-478; (b) fragments of the polypeptides of (a) wherein said fragments have apyrase activity; (c) variants of the polypeptides of (a) or (b), wherein said variants have apyrase activity; and (d) fusion polypeptides comprising the polypeptides of (a), (b),

or (c), wherein said fusion polypeptides have apyrase activity. The invention provides compositions comprising a pharmaceutically acceptable carrier and a soluble CD39 polypeptide.

The invention is also directed to nucleic acids encoding a soluble CD39 polypeptide. The invention provides DNAs, vectors, recombinant cells, and recombinant methods for the production of soluble CD39 polypeptides.

The invention is further directed to the use of soluble CD39 polypeptides for inhibiting platelet activation and recruitment, for inhibiting angiogenesis, or for degrading nucleoside tri- and/or di- phosphates in a mammal in need of such treatment. The invention encompasses the use of a soluble CD39 polypeptide for the preparation of a medicament for inhibiting platelet activation and platelet recruitment, for inhibiting angiogenesis, or for degrading nucleoside tri- and/or di- phosphates in a mammal in need of such treatment. These and other aspects of the present invention will become evident upon reference to the following drawings, examples, and detailed description.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the predicted amino acid sequence (SEQ ID NO:2) of human CD39. The predicted amino acid sequence contains 6 potential N-linked glycosylation sites (double underline), and 11 cysteine residues (bold face). The two predicted transmembrane regions are underlined (single underline).

Figure 2 shows the domain structure of full length CD39 and of an engineered soluble form of CD39. The locations of transmembrane regions near the amino- and carboxy-termini, the centrally located hydrophobic sequence, and a section containing the four putative apyrase conserved regions (ACR) are indicated. Cysteine residues are marked as "C". The soluble CD39 contains a FLAG[®] peptide and new leader sequence and lacks the two transmembrane regions.

Figure 3 shows the immunoaffinity depletion of solCD39 from COS-1 conditioned medium (CM) following one (1X) or two (2X) rounds of adsorption. Samples were assayed for ATPase activity as described in Example 7. Data are expressed as pmoles of ATP degraded per minute.

Figure 4 shows the immunoprecipitation of solCD39 from COS-1 CM. Lane 2 shows the material that specifically bound to the antibody-coated beads. Lane 1 shows material that was pre-incubated with ovalbumin-coated beads to remove non-specifically bound material prior to addition of Ab-coated beads. Migration of molecular weight standards is indicated in kilodaltons (kDa).

Figure 5 shows the immunoaffinity purification and characterization of soluble CD39 (solCD39). Figure 5A shows fractions from the immunoaffinity column analyzed by SDS-PAGE, Figure 5B shows enzyme activity in the fractions, and Figure 5C shows purified solCD39 before (Lane 1) and after (Lane 2) treatment with N-glycanase.

Figure 6A shows pH optimum profiles of HUVEC membrane ecto-ADPase (●) and recombinant solCD39 (■). Figure 6B shows is an Eadie-Hofstee plot of rates of metabolism at different concentrations of ATP (●) or ADP (■) using purified solCD39 (6.5 ng).

Figure 7 shows inhibition of ADP-induced platelet reactivity by purified solCD39 in platelet-rich plasma from a donor who had ingested aspirin. The response to increasing concentrations of ADP is shown in Fig. 7A. The effect of increasing quantities of purified solCD39 on the platelet aggregation response to 10 μ M ADP is shown in Fig. 7B. Arrows indicate the addition of agonist.

5 Data are presented as relative light transmission vs. time (4 min duration).

Figure 8 shows a comparison of platelet reactivity as modulated by different agonists and inhibitors. The effects of CM from cells expressing solCD39 on platelet aggregation induced by 5 μ M ADP (Fig. 8A) and collagen (Fig. 8B) were compared in PRP and PRP treated with 10 μ M indomethacin. In Fig. 8B, 1 μ g/ml collagen was used in the upper samples and 3.3 μ g/ml in the lower (indomethacin-treated) samples. Fig. 8C shows the inhibition of collagen-induced aggregation by increasing quantities of solCD39 in PRP from a donor who had ingested aspirin. The arrows indicate the addition of agonist. Data are presented as relative light transmission vs time (4 min.).

Figure 9 shows the effect of FSBA-treated solCD39 on platelet reactivity. Fig. 9A shows the effects of purified solCD39, FSBA-treated solCD39, and mock-treated solCD39 (each at 4.4 μ g/ml) on ASA-treated PRP after addition of 10 μ M ADP. Fig. 9B shows the effects of FSBA-treated solCD39 and mock-treated solCD39 (each at 22 μ g/ml) on ASA-treated PRP following addition of 3.3 μ g/ml collagen. Fig. 9C shows the titration of mock-treated solCD39 (0.88-2.2 μ g/ml) against FSBA-treated solCD39 (22 μ g/ml). ASA-treated PRP was stimulated with 10 μ M ADP. Arrows indicate addition of agonist. Data are presented as relative light transmission vs time.

20 Figure 10 shows pharmacokinetic analyses of solCD39 in mice. CD39 in serum was measured in the radioactive phosphate release ATPase assay (■) or the ADPase assay (●). Activities are expressed as pmoles nucleotide degraded per minute. The dashed line indicates the ATPase activity of 25 μ g/ml of solCD39 in murine serum. Distribution ($t_{1/2}\alpha = 59$ min (ATP); 43 min (ADP)) and clearance ($t_{1/2}\beta = 40$ h (ATP & ADP)) half-lives were determined using a biphasic curve fit.

25 Figure 11 shows bleeding times at 0 and 60 minutes in pigs treated with low, medium, or high doses of solCD39.

Figure 12 shows the effect of aspirin on pig platelet aggregation at baseline and day 5 after intravenous administration (Fig. 12A) and the effect of effect of high dose solCD39 on platelet aggregation at baseline and day 7 (Fig. 12B).

30 Figure 13 shows the inhibition of pig platelet aggregation by low, medium, and high doses of solCD39 as a function of time after bolus administration.

Figure 14 shows the concentration of CD39 in pig serum as a function of time after low, medium, or high dose administration. Distribution ($t_{1/2}\alpha = 29$ min) and clearance ($t_{1/2}\beta = 51$ h) half-lives were determined using a biphasic curve fit.

35 Figure 15 shows the ex vivo aggregation of murine platelets. Platelets were stimulated with 10 μ M ADP (Fig. 15A), 2.5 μ g/ml collagen (Fig. 15B), or 0.1 mM sodium arachidonate (Fig. 15C) after the administration of vehicle (saline), soluble CD39 (4 mg/kg) or aspirin (5 mg/kg). Soluble

CD39 treatment produced aggregation curves that returned to baseline following stimulation with agonists, but aspirin treatment yielded such a pattern only when arachidonate was the agonist.

Figure 16 shows reversal of the ADP-induced aggregation response in murine platelets when solCD39 is added at the peak of the aggregation response.

Figure 17 shows the inhibition of platelet (n=20, Fig. 17A) and fibrin (n=3, Fig. 17B) deposition following induction of stroke in mice pretreated with 8 mg/kg soluble CD39. "Fibrin" is a positive control, "Ipsilat" is ipsilateral (i.e., the ischemic hemisphere), and "Contralat" is the nonischemic hemisphere.

Figure 18 shows the comparative effects of vehicle (n=23), soluble CD39 (n=67) and aspirin (n=27) on the outcome of induced stroke in mice. Fig. 18A shows cerebral blood flow, 18B shows cerebral infarct volume, 18C shows neurological score (where higher scores indicate a worse deficit (Connolly, E.S., Jr., et al., Neurosurg. 38(3):523-532 (1996)), 18D shows mortality, and 18E shows intracerebral hemorrhage. *p<0.05, †p<0.01, ‡p<0.001.

Figure 19 shows a covariate plot of cerebral infarct volume vs. intracerebral hemorrhage. Vehicle (saline), aspirin (ASA, 5 mg/kg prior to stroke), soluble CD39 (4 & 8 mg/kg, prior to stroke), and soluble CD39 (8 mg/kg, 3 h following stroke induction in mice) are compared.

Figure 20A shows the construct used to generate CD39^{-/-} mice by homologous recombination. The labeled restriction sites are *Bgl*III (B), *Spe*I (S), and *Asp*718 (A). Figure 20B shows a genomic Southern blot as used to identify ES clones having a disrupted CD39 allele.

Figure 21 shows the bleeding times in control (n=15), aspirin-treated (5 mg/kg, n=10), solCD39-treated (4, 8, and 20 mg/kg, n=25) and solCD39^{-/-} mice (n=10). (*p<0.05, †p<0.01, ‡p<0.001).

Figure 22 shows a comparison of stroke outcomes in control (C57BL/6J x 129/J F1) mice (n=6), CD39^{-/-} mice (n=5), and CD39^{-/-} mice which were "reconstituted" with solCD39 (n=6). Figure 22A shows cerebral blood flow, 22B shows cerebral infarct volume, 22C shows neurological score, 22D shows mortality, and 22E shows intracerebral hemorrhage. *p<0.05, †p<0.01, ‡p<0.001.

Figure 23 is a Kaplan-Meier plot showing that solCD39 causes an improvement in survival in a stringent lung ischemia-reperfusion model.

Figure 24 shows an alignment of the N-terminal amino acid sequences of human CD39 and human CD39-L4.

DETAILED DESCRIPTION OF THE INVENTION

A cDNA encoding the cell-surface molecule CD39 has been isolated, cloned and sequenced. The nucleic acid sequence and predicted amino acid sequence of this cDNA are shown in SEQ ID NO:1 and SEQ ID NO:2. The present invention provides methods of using soluble forms of CD39, which were constructed by removing the amino- and carboxy-terminal transmembrane domains. Soluble CD39 retains the capacity of wildtype CD39 to metabolize ATP and ADP at physiologically relevant concentrations as well as the ability to block and reverse ADP-induced platelet activation and

recruitment, including platelet aggregation. The use of soluble forms of CD39 is advantageous because purification of the polypeptides from recombinant host cells is facilitated, and because soluble polypeptides are generally more suitable than membrane-bound forms for clinical administration. Because CD39 inhibits platelet activation and recruitment, and therefore platelet aggregation, the present invention provides methods and compositions for inhibiting formation of a thrombus at a site in a mammal at which platelets are inappropriately activated, methods for use in controlling platelet reactivity, thereby regulating the hemostatic and thrombotic processes, and methods of inhibiting and/or reversing platelet aggregation.

A. Hemostasis

Hemostasis is defined as the arrest of bleeding from damaged blood vessels, and results from a sequence of physiologic and biochemical events. At least three interacting biological systems are involved in hemostasis: components of the blood vessels (such as the subendothelial matrix), platelets, and plasma proteins (Marcus, A.J.: Disorders of Hemostasis, Ratnoff and Forbes, eds., W.B. Saunders, Philadelphia, 1996; pages 79-137; Marcus, A.J.: Platelet Activation, in: Atherosclerosis and Coronary Artery Disease, vol.1, Fuster, Ross and Topol, eds., Lipincott-Raven, Philadelphia, 1996; pages 607-637). A defect or defects in one or more of these systems can result in hemorrhagic disorder; conversely, the inappropriate activation of hemostasis culminates in development of arterial or venous thrombosis.

When a blood vessel is injured, it contracts, exposing subendothelial matrix components such as collagen, von Willebrand factor, fibronectin, thrombospondin, laminin, and microfibrils. Platelets adhere to, and are activated by, these components; collagen is an especially effective agonist for platelet activation. At least four physiologic events are initiated by platelet-collagen contact: the platelets release biologically active compounds; they express P-selectin on their cell surface (where it mediates adhesion of neutrophils, monocytes and subsets of lymphocytes); the platelet eicosanoid pathway is activated (starting with the liberation of arachidonic acid which forms prostaglandin H_2); and the platelets undergo a drastic change in shape, from smooth disks to spiny spheres.

The biologically active compounds released by platelets are numerous, and multi-functional. Included in this group of components are serotonin, ATP, ADP, calcium, adhesive proteins (fibrinogen, fibronectin, thrombospondin, vitronectin, von Willebrand factor), growth factors (platelet-derived growth factor, transforming growth factor- β , platelet factor 4) and coagulation factors (factor V, high-molecular weight kininogen, factor XI, protein S and plasminogen activator inhibitor-I (PAI-I)). Some of these compounds play a role in the recruitment of additional platelets and/or other cells such as neutrophils and monocytes to the site of activation, whereas others are involved in feedback mechanisms to down-regulate excessive thrombus formation.

At least three separate endothelial thromboregulatory systems exist: the eicosanoids including the prostaglandins PGI_1 and PGD_2 ; endothelium-dependent relaxing factor (EDRF/NO); and the ectonucleotidase ATP-diphosphohydrolase (ATPDase) which has both ADPase and ATPase activities.

While collagen and thrombin are the prime inducers of platelet secretion, ADP is the most important agonist of platelet aggregation present in the platelet releasate. Catabolism of ADP to AMP by the ecto-ADPase blocks further recruitment of additional platelets to the site, reverses the aggregation response and blocks subsequent thrombus response.

5 Ecto-nucleotidase activity is demonstrable in vitro in an aggregometry system in which EDRF/NO effects and PGI₂ production are blocked by hemoglobin and aspirin respectively (Marcus and Safier, *FASEB J* 7:516; 1993). In this system, loss of platelet stimulatory activity in the supernatant fluid correlates with ADP catabolism. An ADPase activity has been identified in the membrane fraction of human endothelial cells; enzyme activity detected by polyacrylamide gel
10 electrophoresis indicated both ATPase and ADPase (Marcus et al., *Clin. Res.* 40:226A (abstract), 1992).

B. Utility of the Claimed Invention

15 Significant research efforts are directed to the discovery and characterization of platelet aggregation inhibitors because of the potential utility of such inhibitors in treating occlusive vascular disease. For example, WO 95/12412 discloses platelet-specific chimeric antibodies and methods of using the same in treating various thrombotic disorders. A prototype description of the efforts to develop this therapeutic agent and obtain approval for its use as a human therapeutic agent (generic name: abciximab, trade name: ReoPro®) was described by B.S. Coller in *Circulation* 92:2373 (1995).

20 CD39 is an ecto-ADPase (apyrase) located on the surface of endothelial cells. This enzyme is mainly responsible for the maintenance of blood fluidity, thus maintaining platelets in the baseline (resting) state. This is accomplished by metabolism of the major platelet agonist, adenosine diphosphate, to adenosine monophosphate, which is not an agonist. Because ADP is the most important agonist of platelet aggregation, and is present in platelet releasate, a substance which
25 catabolizes ADP is useful in treating or preventing disease states that involve inappropriate aggregation of platelets.

Examples of the therapeutic uses of soluble CD39 and compositions thereof include the treatment of individuals who suffer from coronary artery disease or injury following myocardial infarction, atherosclerosis, arteriosclerosis, preeclampsia, embolism, platelet-associated ischemic
30 disorders including lung ischemia, coronary ischemia, and cerebral ischemia, and for the prevention of reocclusion following thrombosis, thrombotic disorders including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, and thrombosis and coagulopathies associated with exposure to a foreign or injured tissue surface, in combination with angioplasty, carotid endarterectomy, anastomosis of vascular grafts, and chronic
35 cardiovascular devices such as in-dwelling catheters or shunts. Other instances in which it would be useful to inhibit increased ADP release due to increased platelet stimulation would be in individuals at high risk for thrombus formation or reformation (severe arteriosclerosis), and inhibition of occlusion, reocclusion, stenosis and/or restenosis of blood vessels. Individuals who will benefit from therapies

that involve inhibiting ADP-induced aggregation of platelets include those at risk for advanced coronary artery disease, and those that are or will be undergoing angioplasty procedures (i.e., balloon angioplasty, laser angioplasty, coronary atherectomy and similar techniques). Inhibition of platelet aggregation will also be useful in individuals undergoing surgery that has a high risk of thrombus formation (i.e., coronary bypass surgery, insertion of a prosthetic valve or vessel and the like), and in the prevention or treatment of deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischemic attacks (TIAs) and other related conditions where arterial occlusion is the common underlying feature. In addition, the ability of CD39 to block platelet activation and recruitment is useful for preventing stroke and for treating patients experiencing stroke due to vascular occlusion. In particular, the methods, compounds, and compositions of the present invention have the ability to inhibit microvascular thrombosis, improve postischemic cerebral blood flow, and reduce cerebral infarction volumes and neurological deficit without inducing intracerebral hemorrhage, in stroke. Soluble CD39 and compositions thereof according to the present invention can also be administered in any other therapeutic setting where it would be useful to degrade nucleoside tri- and/or diphosphates. As an example, soluble CD39 may be used as an anti-neoplastic agent to inhibit angiogenesis and/or prevent the survival benefits that ATP provides to tumor cells, or to treat other diseases or conditions mediated by angiogenesis such as ocular neovascularization.

Soluble CD39 polypeptides also have many non-therapeutic uses, since they may be used in any application where soluble ATPase and/or ADPase activity is advantageous. As an example, soluble CD39 polypeptides may be used in compositions for preserving platelets such as those described by Gepner-Puszkun (U.S. Patent No. 5,378,601). As another example, soluble CD39 polypeptides may be used in pyrophosphate-based DNA sequencing methodologies such as those described by Ronaghi et al. (*Science* 281:336, 1998). As a further example, soluble CD39 polypeptides can be used to screen for apyrase inhibitors.

C. CD39 Polypeptides

The molecular cloning and structural characterization of CD39 is presented in Maliszewski et al. (*J. Immunol.* 153:3574, 1994). CD39 contains two putative transmembrane regions, near the amino and carboxy termini, which may serve to anchor the native protein in the cell membrane. The portion of the molecule between the transmembrane regions is external to the cell. As used herein, the term "CD39 polypeptides" includes CD39, homologs of CD39, variants, fragments, and derivatives of CD39, fusion polypeptides comprising CD39, and soluble forms of CD39 polypeptides.

Soluble polypeptides are polypeptides that are capable of being secreted from the cells in which they are expressed. A secreted soluble polypeptide may be identified (and distinguished from its non-soluble membrane-bound counterparts) by separating intact cells which express the desired polypeptide from the culture medium, e.g., by centrifugation, and assaying the medium (supernatant) for the presence of the desired polypeptide. The presence of the desired polypeptide in the medium

indicates that the polypeptide was secreted from the cells and thus is a soluble form of the polypeptide. The use of soluble forms of CD39 is advantageous for many applications. Purification of the polypeptides from recombinant host cells is facilitated, since the soluble polypeptides are secreted from the cells. Moreover, soluble polypeptides are generally more suitable than membrane-bound forms for parenteral administration and for many enzymatic procedures.

Apyrase activity resides in the extracellular domain of CD39. Thus, for applications requiring biological activity, useful CD39 polypeptides include soluble forms of CD39 such as those having an amino terminus selected from the group consisting of amino acids 36-44 of SEQ ID NO:2, and a carboxy terminus selected from the group consisting of amino acids 471-478 of SEQ ID NO:2, and which exhibit CD39 biological activity. Soluble CD39 polypeptides also include those polypeptides which include part of either or both of the transmembrane regions, provided that the soluble CD39 polypeptide is capable of being secreted from a cell, and retains CD39 biological activity. Soluble CD39 polypeptides further include oligomers or fusion polypeptides comprising the extracellular portion of CD39, and fragments of any of these polypeptides that have biological activity.

The term "biological activity," as used herein, includes apyrase enzymatic activity as well as the ex vivo and in vivo activities of CD39. Apyrases catalyze the hydrolysis of nucleoside tri- and/or di-phosphates, but a given apyrase may display different relative specificities for either nucleoside triphosphates or nucleoside diphosphates. Biological activity of soluble forms of CD39 may be determined, for example, in an ectonucleotidase or apyrase assay (e.g. ATPase or ADPase assays), or in an assay that measures inhibition of platelet aggregation. Exemplary assays are disclosed herein; those of skill in the art will appreciate that other, similar types of assays can be used to measure biological activity.

Among the soluble CD39 polypeptides provided herein are variants (also referred to as analogs) of native CD39 polypeptides that retain a biological activity of CD39. Such variants include polypeptides that are substantially homologous to native CD39, but which have an amino acid sequence different from that of a native CD39 because of one or more deletions, insertions or substitutions. Particular embodiments include, but are not limited to, CD39 polypeptides that comprise from one to ten deletions, insertions or substitutions of amino acid residues, when compared to a native CD39 sequence. The CD39-encoding DNAs of the present invention include variants that differ from a native CD39 DNA sequence because of one or more deletions, insertions or substitutions, but that encode a biologically active polypeptide. Included as variants of CD39 polypeptides are those variants that are naturally occurring, such as allelic forms and alternatively spliced forms, as well as variants that have been constructed by modifying the amino acid sequence of a CD39 polypeptide or the nucleotide sequence of a nucleic acid encoding a CD39 polypeptide.

Generally, substitutions for one or more amino acids present in the native polypeptide should be made conservatively. Examples of conservative substitutions include substitution of amino acids outside of the active domain(s), and substitution of amino acids that do not alter the secondary and/or tertiary structure of CD39. Additional examples include substituting one aliphatic residue for another,

such as Ile, Val, Leu, or Ala for one another, or substitutions of one polar residue for another, such as between Lys and Arg; Glu and Asp; or Gln and Asn. Other such conservative substitutions, for example, substitutions of entire regions having similar hydrophobicity characteristics, are known in the art.

When a deletion or insertion strategy is adopted, the potential effect of the deletion or insertion on biological activity must be considered. Subunits of the inventive polypeptides may be constructed by deleting terminal or internal residues or sequences. Additional guidance as to the types of mutations that can be made is provided by a comparison of the sequence of CD39 to polypeptides that have similar structures, as well as by performing structural analysis of the inventive polypeptides.

The native sequence of full length CD39 is set forth in Figure 1 (SEQ ID NO:2). In some preferred embodiments the CD39 variants are at least about 70% identical in amino acid sequence to the amino acid sequence of native CD39 as set forth in the sequence listing; in some preferred embodiments the CD39 variants are at least about 80% identical in amino acid sequence to the amino acid sequence of native CD39 as set forth in the sequence listing. In some more preferred embodiments the variants of CD39 are at least about 90% identical in amino acid sequence to the amino acid sequence of native CD39 as set forth in the sequence listing; in some more preferred embodiments the variants of CD39 are at least about 95% identical in amino acid sequence to the amino acid sequence of native CD39 as set forth in the sequence listing. In some most preferred embodiments, variants of CD39 are at least about 98% identical in amino acid sequence to the amino acid sequence of native CD39 as set forth in the sequence listing; in some most preferred embodiments, variants of CD39 are at least about 99% identical in amino acid sequence to the amino acid sequence of native CD39 as set forth in the sequence listing. Percent identity, in the case of both polypeptides and nucleic acids, may be determined by visual inspection. Percent identity may be determined using the alignment method of Needleman and Wunsch (J. Mol. Biol. 48:443, 1970) as revised by Smith and Waterman (Adv. Appl. Math 2:482, 1981. Preferably, percent identity is determined by using a computer program, for example, the GAP computer program version 10.x available from the Genetics Computer Group (GCG; Madison, WI, see also Devereux et al., *Nucl. Acids Res.* 12:387, 1984). The preferred default parameters for the GAP program include: (1) a unary comparison matrix (containing a value of 1 for identities and 0 for non-identities) for nucleotides, and the weighted comparison matrix of Gribskov and Burgess, *Nucl. Acids Res.* 14:6745, 1986, as described by Schwartz and Dayhoff, eds., *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, pp. 353-358, 1979 for amino acids; (2) a penalty of 30 (amino acids) or 50 (nucleotides) for each gap and an additional 1 (amino acids) or 3 (nucleotides) penalty for each symbol in each gap; (3) no penalty for end gaps; and (4) no maximum penalty for long gaps. Other programs used by one skilled in the art of sequence comparison may also be used. For fragments of CD39, the percent identity is calculated based on that portion of CD39 that is present in the fragment.

The primary amino acid structure of soluble CD39 may be modified to create CD39 derivatives by forming covalent or aggregative conjugates with other chemical moieties, such as glycosyl groups, lipids, phosphate, acetyl groups and the like. Covalent derivatives of CD39 are prepared by linking particular functional groups to CD39 amino acid side chains or at the N-terminus or C-terminus of a CD39 polypeptide or the extracellular domain thereof. CD39 derivatives also include CD39 polypeptides bound to various insoluble substrates, including cyanogen bromide-activated agarose structures, or similar agarose structures, or adsorbed to polyolefin surfaces (with or without glutaraldehyde cross-linking).

Fusion polypeptides of soluble CD39 within the scope of this invention include covalent or aggregative conjugates of CD39 or its fragments with other polypeptides, such as by synthesis in recombinant culture as N-terminal or C-terminal fusions. One class of fusion polypeptides are discussed below in connection with soluble CD39 oligomers. As another example, a fusion polypeptide may comprise a signal peptide (which is also variously referred to as a signal sequence, signal, leader peptide, leader sequence, or leader) at the N-terminal region or C-terminal region of a CD39 polypeptide which co-translationally or post-translationally directs transfer of the polypeptide from its site of synthesis to a site inside or outside of the cell membrane or cell wall (e.g. the α -factor leader of *Saccharomyces*; several leader sequences are discussed in the examples that follow). It is particularly advantageous to fuse a signal peptide that promotes extracellular secretion to the N-terminus of a soluble CD39 polypeptide. In this case, the signal peptide is typically cleaved upon secretion of the soluble CD39 from the cell.

In a particularly preferred embodiment, one or more amino acids are added to the N-terminus of a soluble CD39 polypeptide in order to improve the expression levels and/or stability of the CD39 polypeptide. The one or more amino acids include an Ala residue, fragments derived from the N-terminus of another member of the CD39 family (e.g., CD39L2, CD39L3, CD39L4) or from another polypeptide such as IL-2, and other peptides, either naturally-occurring or designed based upon structural predictions, capable of adopting a stable secondary structure.

In a most preferred embodiment, a soluble CD39 polypeptide is initially synthesized as a fusion polypeptide comprising: (a) a signal peptide that promotes extracellular secretion of the soluble CD39 from the cell, the signal peptide being cleaved upon secretion, (b) one or more amino acids added to the N-terminus of the soluble CD39 polypeptide in order to improve expression levels and/or stability, and (c) a fragment of CD39 that possesses biological activity.

CD39 fusion polypeptides can also comprise polypeptides added to provide novel polyfunctional entities. Further, soluble CD39-containing fusion polypeptides can comprise peptides added to facilitate purification and identification of soluble CD39. Such peptides include, for example, poly-His or the antigenic identification peptides described in U.S. Patent No. 5,011,912 and in Hopp et al., *Bio/Technology* 6:1204, 1988. One such peptide is the FLAG[®] peptide, Asp-Tyr-Lys-Asp-Asp-Asp-Lys (SEQ ID NO:10), which is highly antigenic and provides an epitope reversibly

bound by a specific monoclonal antibody, enabling rapid assay and facile purification of expressed recombinant polypeptide. A murine hybridoma designated 4E11 produces a monoclonal antibody that binds the FLAG[®] peptide in the presence of certain divalent metal cations, as described in U.S. Patent 5,011,912, hereby incorporated by reference. The 4E11 hybridoma cell line has been deposited with the American Type Culture Collection under accession no. HB 9259. Monoclonal antibodies that bind the FLAG[®] peptide are available from Eastman Kodak Co., Scientific Imaging Systems Division, New Haven, Connecticut.

Another particularly useful class of fusion polypeptides includes those that allow localization or concentration of CD39 at a site of platelet activation and recruitment. Such fusion polypeptides comprise a moiety that specifically binds activated platelets and CD39, and can be prepared using recombinant DNA technology, or by using standard techniques for conjugation of polypeptides. For example, WO 95/12412 discloses platelet-specific chimeric antibodies and methods of using the same in treating various thrombotic disorders. These antibodies, or other platelet specific antibodies (for example, antibodies to P-selectin/CD62), are useful in forming fusion polypeptides with CD39. Moreover, humanized or single chain antibodies can be prepared, based on such platelet specific antibodies.

Counterstructure molecules (molecules that specifically bind polypeptides expressed on the cell surface of activated platelets) and fragments thereof that bind to platelets are also useful in forming fusion polypeptides that bind specifically to activated platelets. Exemplary counterstructures include ligands for P-selectin/CD62 (see, i.e., Varki A., *Proc Natl Acad Sci U S A* 91:7390, 1994; Sammar et al., *Int Immunol* 6:1027, 1994; Lenter et al., *J Cell Biol* 125:471, 1994).

Encompassed by the present invention are oligomers that contain CD39 polypeptides. CD39 oligomers may be in the form of covalently-linked or non-covalently-linked multimers, including dimers, trimers, or higher oligomers. Oligomers may be linked by disulfide bonds formed between cysteine residues on different CD39 polypeptides. Alternatively, oligomers may be formed by constructing fusion polypeptides of CD39 and the Fc region of an immunoglobulin molecule, such as human IgG₁, to yield a CD39/Fc fusion polypeptide. The term "Fc polypeptide" as used herein includes native and mutein forms of polypeptides derived from the Fc region of an antibody.

Truncated forms of such polypeptides containing the hinge region that promotes dimerization are also included. One suitable Fc polypeptide, described in PCT application WO 93/10151 (hereby incorporated by reference), is a single chain polypeptide extending from the N-terminal hinge region to the native C-terminus of the Fc region of a human IgG1 antibody. Another useful Fc polypeptide is the Fc mutein described in U.S. Patent 5,457,035 and in Baum et al., (*EMBO J.* 13:3992-4001, 1994). The amino acid sequence of this mutein is identical to that of the native Fc sequence presented in WO 93/10151, except that amino acid 19 has been changed from Leu to Ala, amino acid 20 has been changed from Leu to Glu, and amino acid 22 has been changed from Gly to Ala. The mutein exhibits reduced affinity for Fc receptors. The CD39/Fc fusion polypeptides are allowed to assemble much

like heavy chains of an antibody molecule to form divalent CD39. If fusion polypeptides are made with both heavy and light chains of an antibody, it is possible to form a CD39 oligomer with as many as four CD39 extracellular regions.

In some embodiments of the invention, oligomers comprising multiple CD39 polypeptides are joined via covalent or non-covalent interactions between peptide moieties fused to the C39-polypeptides. Such peptide moieties may be peptide linkers (spacers), or peptides that have the property of promoting oligomerization. Leucine zippers and certain polypeptides derived from antibodies are among the peptides that can promote oligomerization of polypeptides.

The present invention comprises fusion polypeptides with or without spacer amino acid linking groups. For example, two soluble CD39 domains can be linked with a linker sequence, such as (Gly)₄Ser(Gly)₅Ser, which is described in United States Patent 5,073,627. Other linker sequences include, for example, GlyAlaGlyGlyAlaGlySer(Gly)₅Ser, (Gly₄Ser)₂, (GlyThrPro)₃, and (Gly₄Ser)₃Gly₄SerGly₅Ser. Alternatively, CD39 can be linked to another polypeptide (non-CD39) with or without a spacer amino acid linking group. As shown in Example 9, ThrSerSer or ThrSerSerGly linkers may be used to fuse IL2 residues to soluble CD39. For the expression of soluble CD39, the inventors have made the surprising and unexpected discovery that the fusion of 12 amino acids from the N-terminus of mature human IL2 to the solCD39 coding region, results in high levels of both expression and activity in the supernatants of transfected cells. Among the particularly preferred embodiments of the invention, therefore, are soluble CD39 polypeptides having an amino acid sequence SEQ ID NO:6 and nucleic acids, such as SEQ ID NO:5, that encode soluble CD39 polypeptides having an amino acid sequence SEQ ID NO:6.

The present invention further includes soluble CD39 polypeptides with or without associated native-pattern glycosylation. CD39 expressed in yeast or mammalian expression systems (e.g., COS-7 cells) may be similar to or significantly different from a native CD39 polypeptide in molecular weight and glycosylation pattern, depending upon the choice of expression system. Expression of CD39 polypeptides in bacterial expression systems, such as *E. coli*, provides non-glycosylated molecules.

Different host cells may process polypeptides differentially, resulting in heterogeneous mixtures of polypeptides with variable N- or C-termini. Expression of soluble CD39 polypeptides in microbial expression systems, such as *E. coli*, generally provides a homogeneous polypeptide preparation. Polypeptides may be differentially processed by a eukaryotic cell, resulting in variable N- and C-termini, and hence yield a heterogeneous polypeptide preparation. The present invention includes polypeptides, produced by eukaryotic host cells, which have variable N-termini or C-termini. In one embodiment of the inventive CD39 polypeptides, the amino and carboxy termini can be about five amino acids different from those disclosed herein.

The skilled artisan will also recognize that the position(s) at which a signal peptide is cleaved may differ from that predicted by computer program, and may vary according to such factors as the type of host cells employed in expressing a recombinant soluble CD39 polypeptide. A polypeptide

preparation according to the invention may therefore include a mixture of polypeptide molecules having different N-terminal amino acids, resulting from cleavage of the signal peptide at more than one site.

D. Nucleic Acids

5 The invention encompasses full length nucleic acid molecules encoding soluble CD39 as well as isolated fragments and oligonucleotides derived from the nucleotide sequence of SEQ ID NO:1. Such nucleic acid sequences may include nucleotides 178-1494 of SEQ ID NO:1 or a fragment thereof, and DNA and/or RNA sequences that hybridize to the coding region of the nucleotide sequence of SEQ ID NO:1, or its complement, under conditions of moderate stringency, and which
10 encode polypeptides or fragments thereof of the invention.

 Nucleic acid sequences encoding soluble CD39 polypeptides having altered glycosylation sites, deleted or substituted Cys residues, or modified proteolytic cleavage sites, nucleic acid sequences encoding sub-units of CD39 polypeptides or fusion polypeptides of CD39 with other peptides, allelic variants of CD39, mammalian homologs of CD39, and nucleic acid sequences
15 encoding CD39 polypeptides derived from alternative mRNA constructs, or those that encode peptide having substituted or additional amino acids, are examples of nucleic acid sequences according to the invention.

 Due to degeneracy of the genetic code, there can be considerable variation in nucleotide sequences encoding the same amino acid sequence. Included as embodiments of the invention are
20 sequences capable of hybridizing under moderately stringent conditions (e.g., prewashing solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0) and hybridization conditions of 50°C, 5 X SSC, overnight) to the DNA sequences encoding soluble CD39, and other sequences which are degenerate to those which encode soluble CD39. The skilled artisan can determine additional combinations of salt and temperature that constitute moderate hybridization stringency. Conditions of higher
25 stringency include higher temperatures for hybridization and post-hybridization washes, and/or lower salt concentration.

 In a preferred embodiment, CD39 DNAs include those that encode polypeptides that are at least about 70% or at least 80% identical in amino acid sequence to the amino acid sequence of native CD39 polypeptide as set forth in SEQ ID NO:1. In a more preferred embodiment, the encoded
30 variants of CD39 are at least about 90% or at least about 95% identical in amino acid sequence to the native form of CD39; in a most preferred embodiment, the encoded variants of CD39 are at least about 98% or at least about 99% identical in amino acid sequence to the native form of CD39. For DNAs that encode a fragment of CD39, percent identity of the fragment is based on percent identity to the corresponding portion of full-length CD39.

35 Mutations can be introduced into nucleic acids by synthesizing oligonucleotides containing a mutant sequence, flanked by restriction sites enabling ligation to fragments of the native sequence.

Following ligation, the resulting reconstructed sequence encodes a variant having the desired amino acid insertion, substitution, or deletion.

Alternatively, oligonucleotide-directed site-specific mutagenesis procedures can be employed to provide an altered gene having particular codons altered according to the substitution, deletion, or insertion required. Exemplary methods of making the alterations set forth above are disclosed by Walder et al. (*Gene* 42:133, 1986); Bauer et al. (*Gene* 37:73, 1985); Craik (*BioTechniques*, January 1985, 12-19); Smith et al. (*Genetic Engineering: Principles and Methods*, Plenum Press, 1981); and U.S. Patent Nos. 4,518,584 and 4,737,462 disclose suitable techniques, and are incorporated by reference herein.

The well known polymerase chain reaction (PCR) procedure also may be employed to generate and amplify a DNA sequence encoding a desired polypeptide or fragment thereof. Oligonucleotides that define the desired termini of the DNA fragment are employed as 5' and 3' primers. The oligonucleotides may additionally contain recognition sites for restriction endonucleases to facilitate insertion of the amplified DNA fragment into an expression vector. PCR techniques are described in Saiki et al., *Science* 239:487, 1988; *Recombinant DNA Methodology*, Wu et al., eds., Academic Press, Inc., San Diego, 1989, pp. 189-196; and *PCR Protocols: A Guide to Methods and Applications*, Innis et al., eds., Academic Press, Inc., 1990.

DNA sequences that encode CD39 polypeptides comprising various additions or substitutions of amino acid residues or sequences, or deletions of terminal or internal residues or sequences not needed for biological activity can be prepared. For example, N-glycosylation sites can be modified to preclude glycosylation while allowing expression of a homogeneous, reduced carbohydrate variant using yeast expression systems. N-glycosylation sites in eukaryotic polypeptides are characterized by an amino acid triplet Asn-X-Y, wherein X is any amino acid except Pro and Y is Ser or Thr. Appropriate modifications to the nucleotide sequence encoding this triplet will result in substitutions, additions or deletions that prevent attachment of carbohydrate residues at the Asn side chain.

In another example, sequences encoding Cys residues can be altered to cause the Cys residues to be deleted or replaced with other amino acids, preventing formation of incorrect intramolecular disulfide bridges upon renaturation. Thus, Cys residues may be replaced with another amino acid or deleted without affecting polypeptide tertiary structure or disulfide bond formation.

Other approaches to mutagenesis involve modification of sequences encoding dibasic amino acid residues to enhance expression in yeast systems in which KEX2 protease activity is present. Other variants are prepared by modification of adjacent dibasic amino acid residues, to enhance expression in yeast systems in which KEX2 protease activity is present. EP 212,914 discloses the use of site-specific mutagenesis to inactivate KEX2 protease processing sites in a polypeptide. KEX2 protease processing sites are inactivated by deleting, adding or substituting residues to alter Arg-Arg, Arg-Lys, and Lys-Arg pairs to eliminate the occurrence of these adjacent basic residues. Similar modification may be made to sequences encoding sites recognized and cleaved by other proteolytic enzymes. Subunits of a CD39 polypeptide may be constructed by deleting sequences encoding terminal or internal

residues or sequences not necessary for biological activity. Sequences encoding fusion polypeptides as described below may be constructed by ligating sequences encoding additional amino acid residues to the inventive sequences without affecting biological activity.

5 Mutations in nucleotide sequences constructed for expression of a soluble CD39 must, of course, preserve the reading frame phase of the coding sequences and preferably will not create complementary regions that could hybridize to produce secondary mRNA structures such as loops or hairpins which would adversely affect translation of the receptor mRNA. Although a mutation site may be predetermined, it is not necessary that the nature of the mutation *per se* be predetermined. For example, in order to select for optimum characteristics of mutants at a given site, random mutagenesis
10 may be conducted at the target codon and the expressed mutated polypeptides screened for the desired activity.

Not all mutations in the nucleotide sequence which encodes a CD39 polypeptide will be expressed in the final product, for example, nucleotide substitutions may be made to enhance expression, primarily to avoid secondary structure loops in the transcribed mRNA (see EPA 75,444A,
15 incorporated herein by reference), or to provide codons that are more readily translated by the selected host, e.g., the well-known *E. coli* preference codons for *E. coli* expression.

In the genome, CD39 polypeptides are encoded by multi-exon genes. The present invention further includes alternative mRNA constructs which can be attributed to different mRNA splicing events following transcription and which hybridize with the cDNAs disclosed herein under conditions
20 of moderate stringency. CD39 polypeptides according to the invention include allelic variations of the sequence shown in SEQ ID NO:1, and sequences encoding CD39 polypeptides that comprise additional amino acids to those of SEQ ID NO:1.

The isolated nucleic acid sequences of this invention are sufficiently free of association with nucleic acid sequences encoding other proteinaceous material, and from other materials found in living
25 cells, such as proteins, lipids or carbohydrates, to allow the skilled artisan to prepare vectors for the expression of soluble CD39 polypeptides.

E. Recombinant Expression Systems

The present invention also provides recombinant cloning and expression vectors containing CD39 DNA, as well as host cells containing the recombinant vectors. Expression vectors comprising
30 CD39 DNA may be used to prepare soluble CD39 polypeptides encoded by the DNA. The expression vectors carrying the recombinant CD39 DNA sequence are transferred, for example by transfection or transformation, into a substantially homogeneous culture of a suitable host microorganism or mammalian cell line. Transformed host cells are cells which have been transformed or transfected with nucleotide sequences encoding CD39 polypeptides and express CD39 polypeptides. Expressed
35 CD39 polypeptides will be located within the host cell and/or secreted into culture supernatant fluid, depending upon the nature of the host cell and the gene construct inserted into the host cell. The

skilled artisan will recognize that the procedure for purifying the expressed CD39 will vary according to such factors as the type of host cells employed.

Any suitable expression system may be employed. Recombinant expression vectors for expression of soluble CD39 by recombinant DNA techniques include a CD39 DNA sequence comprising a synthetic or cDNA-derived DNA fragment encoding a CD39 polypeptide, operably linked to a suitable transcriptional or translational regulatory nucleotide sequence, such as one derived from a mammalian, microbial, viral, or insect gene.

Examples of regulatory sequences include transcriptional promoters, operators, or enhancers, an mRNA ribosomal binding site, and appropriate sequences which control transcription and translation initiation and termination. Nucleotide sequences are operably linked when the regulatory sequence functionally relates to the CD39 DNA sequence. Thus, a promoter nucleotide sequence is operably linked to a CD39 DNA sequence if the promoter nucleotide sequence controls the transcription of the CD39 DNA sequence. An origin of replication that confers the ability to replicate in the desired host cells, and a selection gene by which transformants are identified, are generally incorporated into the expression vector.

In addition, a sequence encoding an appropriate signal peptide (native or heterologous) can be incorporated into expression vectors. A DNA sequence for a signal peptide (secretory leader) may be fused in frame to the CD39 sequence so that the CD39 is initially translated as a fusion polypeptide comprising the signal peptide. A signal peptide that is functional in the intended host cells promotes extracellular secretion of the CD39 polypeptide. The signal peptide is cleaved from the CD39 polypeptide upon secretion of soluble CD39 from the cell.

Regarding signal peptides that may be employed in producing soluble CD39, the native signal peptide may be replaced by a heterologous signal peptide or leader sequence, if desired. The choice of signal peptide or leader may depend on factors such as the type of host cells in which the recombinant polypeptide is to be produced. To illustrate, examples of heterologous signal peptides that are functional in mammalian host cells include the signal sequence for interleukin-7 (IL-7) described in United States Patent 4,965,195, the signal sequence for interleukin-2 receptor described in Cosman et al., *Nature* 312:768, 1984; the interleukin-4 receptor signal peptide described in EP 367,566; the type I interleukin-1 receptor signal peptide described in U.S. Patent 4,968,607; and the type II interleukin-1 receptor signal peptide described in EP 460,846. For the expression of soluble CD39, the inventors have made the surprising and unexpected discovery that the use of a leader containing sequences derived from a human IL-2 polypeptide (SEQ ID NO:9) results in high levels of ATPase activity in the supernatants of transfected cells. Among the particularly preferred embodiments of the invention, therefore, are nucleic acids encoding soluble CD39 polypeptides having an amino acid sequence SEQ ID NO:8.

Suitable host cells for expression of CD39 polypeptides include prokaryotes, yeast or higher eukaryotic cells. Mammalian or insect cells are generally preferred for use as host cells. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are

described, for example, in Pouwels et al. *Cloning Vectors: A Laboratory Manual*, Elsevier, New York, 1985. Cell-free translation systems could also be employed to produce soluble CD39 polypeptides using RNAs derived from DNA constructs disclosed herein.

Prokaryotes include gram negative or gram positive organisms, for example, *E. coli* or *Bacilli*. Suitable prokaryotic host cells for transformation include, for example, *E. coli*, *Bacillus subtilis*, *Salmonella typhimurium*, and various other species within the genera *Pseudomonas*, *Streptomyces*, and *Staphylococcus*. In a prokaryotic host cell, such as *E. coli*, polypeptides may include an N-terminal methionine residue to facilitate expression of the recombinant polypeptide in the prokaryotic host cell. The N-terminal Met may be cleaved from the expressed recombinant polypeptide.

Expression vectors for use in prokaryotic host cells generally comprise one or more phenotypic selectable marker genes. A phenotypic selectable marker gene is, for example, a gene encoding a protein that confers antibiotic resistance or that supplies an autotrophic requirement. Examples of useful expression vectors for prokaryotic host cells include those derived from commercially available plasmids such as the cloning vector pBR322 (ATCC 37017). pBR322 contains genes for ampicillin and tetracycline resistance and thus provides simple means for identifying transformed cells. An appropriate promoter and a CD39 DNA sequence are inserted into the pBR322 vector. Other commercially available vectors include, for example, pKK223-3 (Pharmacia Fine Chemicals, Uppsala, Sweden) and pGEM1 (Promega Biotec, Madison, WI, USA).

Promoter sequences commonly used for recombinant prokaryotic host cell expression vectors include β -lactamase (penicillinase), lactose promoter system (Chang et al., *Nature* 275:615, 1978; and Goeddel et al., *Nature* 281:544, 1979), tryptophan (trp) promoter system (Goeddel et al., *Nucl. Acids Res.* 8:4057, 1980; and EP-A-36776) and tac promoter (Maniatis, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory, p. 412, 1982). A particularly useful prokaryotic host cell expression system employs a phage λ P_L promoter and a cI857ts thermolabile repressor sequence. Plasmid vectors available from the American Type Culture Collection which incorporate derivatives of the λ P_L promoter include plasmid pHUB2 (resident in *E. coli* strain JMB9, ATCC 37092) and pPLc28 (resident in *E. coli* RR1, ATCC 53082).

Soluble CD39 may also be expressed in yeast host cells, preferably from the *Saccharomyces* genus (e.g., *S. cerevisiae*). Other genera of yeast, such as *Pichia* or *Kluyveromyces*, may also be employed. Yeast vectors will often contain an origin of replication sequence from a 2 μ yeast plasmid, an autonomously replicating sequence (ARS), a promoter region, sequences for polyadenylation, sequences for transcription termination, and a selectable marker gene. Suitable promoter sequences for yeast vectors include, among others, promoters for metallothionein, 3-phosphoglycerate kinase (Hitzeman et al., *J. Biol. Chem.* 255:2073, 1980) or other glycolytic enzymes (Hess et al., *J. Adv. Enzyme Reg.* 7:149, 1968; and Holland et al., *Biochem.* 17:4900, 1978), such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase,

phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phospho-glucose isomerase, and glucokinase. Other suitable vectors and promoters for use in yeast expression are further described in Hitzeman, EPA-73,657. Another alternative is the glucose-repressible ADH2 promoter described by Russell et al. (*J. Biol. Chem.* 258:2674, 1982) and Beier et al. (*Nature* 300:724, 1982). Shuttle vectors replicable in both yeast and *E. coli* may be constructed by inserting DNA sequences from pBR322 for selection and replication in *E. coli* (Amp^r gene and origin of replication) into the above-described yeast vectors.

The yeast α -factor leader sequence may be employed to direct secretion of recombinant polypeptides. The α -factor leader sequence is often inserted between the promoter sequence and the structural gene sequence. See, e.g., Kurjan et al., *Cell* 30:933, 1982 and Bitter et al., *Proc. Natl. Acad. Sci. USA* 81:5330, 1984. Other leader sequences suitable for facilitating secretion of recombinant polypeptides from yeast hosts are known to those of skill in the art. A leader sequence may be modified near its 3' end to contain one or more restriction sites. This will facilitate fusion of the leader sequence to the structural gene.

Yeast transformation protocols are known to those of skill in the art. One such protocol is described by Hinnen et al., *Proc. Natl. Acad. Sci. USA* 75:1929, 1978. The Hinnen et al. protocol selects for Trp⁺ transformants in a selective medium, wherein the selective medium consists of 0.67% yeast nitrogen base, 0.5% casamino acids, 2% glucose, 10 μ g/ml adenine and 20 μ g/ml uracil.

Yeast host cells transformed by vectors containing an ADH2 promoter sequence may be grown for inducing expression in a "rich" medium. An example of a rich medium is one consisting of 1% yeast extract, 2% peptone, and 1% glucose supplemented with 80 μ g/ml adenine and 80 μ g/ml uracil. Derepression of the ADH2 promoter occurs when glucose is exhausted from the medium.

Mammalian or insect host cell culture systems also may be employed to express recombinant CD39 polypeptides. Bacculovirus systems for production of heterologous polypeptides in insect cells are reviewed by Luckow and Summers, *Bio/Technology* 6:47, 1988. Established cell lines of mammalian origin may also be used. Examples of suitable mammalian host cell lines include the COS-7 line of monkey kidney cells (ATCC CRL 1651) (Gluzman et al., *Cell* 23:175, 1981), L cells, C127 cells, 3T3 cells (ATCC CCL 163), Chinese hamster ovary (CHO) cells, HeLa cells, and BHK (ATCC CRL 10) cell lines, and the CV1/EBNA cell line derived from the African green monkey kidney cell line CV1 (ATCC CCL 70) as described by McMahon et al. (*EMBO J.* 10: 2821, 1991). For the production of therapeutic polypeptides it is particularly advantageous to use a mammalian host cell line which has been adapted to grow in media that does not contain animal proteins. The use of such a cell line for the expression of soluble CD39 is described in Example 13.

Established methods for introducing DNA into mammalian cells have been described (Kaufman, R.J., *Large Scale Mammalian Cell Culture*, 1990, pp. 15-69). Additional protocols using commercially available reagents, such as Lipofectamine (Gibco/BRL) or Lipofectamine-Plus, can be used to transfect cells (Felgner et al., *Proc. Natl. Acad. Sci. USA* 84:7413-7417, 1987). In addition,

electroporation can be used to transfect mammalian cells using conventional procedures, such as those in Sambrook et al. *Molecular Cloning: A Laboratory Manual*, 2 ed. Vol. 1-3, Cold Spring Harbor Laboratory Press, 1989). Selection of stable transformants can be performed using methods known in the art, such as, for example, resistance to cytotoxic drugs. Kaufman et al., *Meth. in Enzymology* 185:487-511, 1990, describes several selection schemes, such as dihydrofolate reductase (DHFR) resistance. A suitable host strain for DHFR selection can be CHO strain DX-B11, which is deficient in DHFR (Urlaub and Chasin, *Proc. Natl. Acad. Sci. USA* 77:4216-4220, 1980). A plasmid expressing the DHFR cDNA can be introduced into strain DX-B11, and only cells that contain the plasmid can grow in the appropriate selective media. Other examples of selectable markers that can be incorporated into an expression vector include cDNAs conferring resistance to antibiotics, such as G418 and hygromycin B. Cells harboring the vector can be selected on the basis of resistance to these compounds.

Transcriptional and translational control sequences for mammalian host cell expression vectors can be excised from viral genomes. Commonly used promoter sequences and enhancer sequences are derived from polyoma virus, adenovirus 2, simian virus 40 (SV40), and human cytomegalovirus. DNA sequences derived from the SV40 viral genome, for example, SV40 origin, early and late promoter, enhancer, splice, and polyadenylation sites can be used to provide other genetic elements for expression of a structural gene sequence in a mammalian host cell. Viral early and late promoters are particularly useful because both are easily obtained from a viral genome as a fragment, which can also contain a viral origin of replication (Fiers et al., *Nature* 273:113, 1978; Kaufman, *Meth. in Enzymology*, 1990). Smaller or larger SV40 fragments can also be used, provided the approximately 250 bp sequence extending from the *Hind* III site toward the *Bgl* I site located in the SV40 viral origin of replication site is included.

Additional control sequences shown to improve expression of heterologous genes from mammalian expression vectors include such elements as the expression augmenting sequence element (EASE) derived from CHO cells (Morris et al., *Animal Cell Technology*, 1997, pp. 529-534) and the tripartite leader (TPL) and VA gene RNAs from Adenovirus 2 (Gingeras et al., *J. Biol. Chem.* 257:13475-13491, 1982). The internal ribosome entry site (IRES) sequences of viral origin allows dicistronic mRNAs to be translated efficiently (Oh and Sarnow, *Current Opinion in Genetics and Development* 3:295-300, 1993; Ramesh et al., *Nucleic Acids Research* 24:2697-2700, 1996). Expression of a heterologous cDNA as part of a dicistronic mRNA followed by the gene for a selectable marker (e.g. DHFR) has been shown to improve transfectability of the host and expression of the heterologous cDNA (Kaufman, *Meth. in Enzymology*, 1990). Exemplary expression vectors that employ dicistronic mRNAs are pTR-DC/GFP described by Mosser et al., *Biotechniques* 22:150-161, 1997, and p2A5I described by Morris et al., *Animal Cell Technology*, 1997, pp. 529-534.

A useful high expression vector, pCAVNOT, has been described by Mosley et al., *Cell* 59:335-348, 1989. Other expression vectors for use in mammalian host cells can be constructed as disclosed by Okayama and Berg (*Mol. Cell. Biol.* 3:280, 1983). A useful system for stable high level

expression of mammalian cDNAs in C127 murine mammary epithelial cells can be constructed substantially as described by Cosman et al. (*Mol. Immunol.* 23:935, 1986). A useful high expression vector, PMLSV N1/N4, described by Cosman et al., *Nature* 312:768, 1984, has been deposited as ATCC 39890. Additional useful mammalian expression vectors are described in EP-A-0367566, and
5 in U.S. Patent Application Serial No. 07/701,415, filed May 16, 1991, incorporated by reference herein. The vectors can be derived from retroviruses. In place of the native signal sequence, a heterologous signal sequence can be added, such as the signal sequence for IL-7 described in United States Patent 4,965,195; the signal sequence for IL-2 receptor described in Cosman et al., *Nature* 312:768, 1984; the IL-4 signal peptide described in EP 367,566; the type I IL-1 receptor signal peptide
10 described in U.S. Patent 4,968,607; and the type II IL-1 receptor signal peptide described in EP 460,846.

Another useful expression vector, pFLAG, can be used. FLAG[®] technology is centered on the fusion of a low molecular weight (1kD), hydrophilic, FLAG[®] marker peptide to the N-Terminus of a recombinant polypeptide expressed by the pFLAG-1[™] Expression Vector (obtained from IBI
15 Kodak).

F. Purification of soluble CD39 Polypeptides

Soluble CD39 polypeptides may be prepared by culturing transformed host cells under culture conditions necessary to express CD39 polypeptides. The resulting expressed polypeptides may then
20 be purified from culture media or cell extracts. Supernatant fluid from the cultured, transformed host cells may be concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. Following the concentration step, the concentrate may be applied to a cation exchange matrix. Suitable cation exchangers include various insoluble matrices comprising sulfonic or carboxymethyl groups; sulfonic groups are preferred. The matrices
25 can be acrylamide, agarose, dextran, cellulose or other types commonly employed in protein purification. Subsequently, an anion exchange resin is employed, for example, a matrix or substrate having pendant diethylaminoethyl (DEAE) or quaternary amino groups; quaternary amino groups are preferred. The matrices can be acrylamide, agarose, dextran, cellulose or other types commonly employed in protein purification. Additionally, a gel filtration medium may be employed to further
30 purify CD39 polypeptides according to approximate molecular weight. Alternatively, certain of these steps may not be performed, or may be performed in the reverse order.

One or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, (e.g., silica gel having pendant methyl or other aliphatic groups) may be employed to further purify CD39. A substantially purified and homogeneous
35 polypeptide having CD39 biological activity may be eluted from a polyacrylamide gel subsequent to electrophoretic separation. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially purified and homogeneous recombinant polypeptide

containing less than about 1% by mass of protein contaminants residual of production processes, or alternatively, which is greater than about 95% pure by gel electrophoresis.

Affinity chromatography may be utilized to purify soluble CD39. Affinity purification of soluble CD39 from conditioned media is described in Example 12C. Moreover, small amounts of purified CD39 may be obtained by immunoprecipitating CD39 with a monoclonal antibody, electrophoresing the immunoprecipitate on a polyacrylamide gel, excising the portion of the gel containing the CD39, and eluting the CD39 from the excised portion of the gel.

Recombinant polypeptides produced in bacterial culture are generally isolated by disruption of the host cells, centrifugation, extraction from cell pellets if an insoluble polypeptide, or from the supernatant fluid if a soluble polypeptide, followed by one or more concentration, salting-out, ion exchange, affinity purification or size exclusion chromatography steps. Finally, RP-HPLC can be employed for final purification steps. Microbial cells can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

Transformed yeast host cells may be employed to express CD39 as a secreted polypeptide. This simplifies purification. Secreted recombinant polypeptide from a yeast host cell fermentation can be purified by methods analogous to those disclosed by Urdal et al. (*J. Chromatog.* 296:171, 1984). Urdal et al. describe two sequential, reversed-phase HPLC steps for purification of recombinant human IL-2 on a preparative HPLC column.

The desired degree of purity of soluble CD39 polypeptides depends on the intended use of the polypeptide. A relatively high degree of purity is desired when the polypeptide is to be administered in vivo, for example. Advantageously, soluble CD39 polypeptides are purified such that no protein bands corresponding to other (non-CD39) polypeptides are detectable upon analysis by SDS-polyacrylamide gel electrophoresis (SDS-PAGE). Following electrophoresis, the protein band may be visualized by silver staining, Coomassie blue staining, or (if the protein is radiolabeled) by autoradiography. It will be recognized by one skilled in the pertinent field that multiple bands corresponding to CD39 polypeptide may be visualized by SDS-PAGE, due to differential glycosylation, differential post-translational processing, and the like.

G. Therapeutic Compositions of CD39 Polypeptides

The present invention provides compositions comprising an effective amount of a soluble CD39 polypeptide in a pharmaceutically acceptable carrier. As used herein, the terms "therapy," "therapeutic," "treat," and "treatment" generally include prophylaxis, i.e., prevention, of a disease or condition in addition to therapy or treatment for an extant disease or condition. Therapeutic compositions of soluble CD39 polypeptides may therefore need to be administered before, during, or after the presentation of symptoms. For therapeutic use, a soluble CD39 polypeptide is administered to a patient for treatment in a manner appropriate to the indication. Thus, for example, soluble CD39 pharmaceutical compositions which are administered to achieve a desired therapeutic effect can be given by bolus injection, continuous infusion, sustained release from implants or the like, or other

suitable technique. Ideally, development of a stable form of CD39 or closely related biologically active variant would allow its use in oral form, a preferable route of administration. Since CD39 is aspirin-insensitive, these two therapeutic agents (CD39 compositions and aspirin) can be used in combination, for maximal benefit.

Typically, a soluble CD39 therapeutic agent will be administered in the form of a pharmaceutical composition comprising purified soluble CD39 in conjunction with physiologically acceptable carriers, including excipients or diluents. Such carriers will be nontoxic to patients at the dosages and concentrations employed. As described in the examples that follow, the administration of CD39 in murine and porcine models of thrombosis does not cause any observable toxic effects.

Moreover, a second dose of CD39 does not evoke any signs of immunogenicity. Ordinarily, the preparation of such compositions entails combining a soluble CD39 composition with buffers, antioxidants such as ascorbic acid, low molecular weight (less than about 10 residues) polypeptides, polypeptides, amino acids, carbohydrates including glucose, sucrose or dextrans, chelating agents such as EDTA, glutathione and other stabilizers and excipients. Neutral buffered saline or saline mixed with conspecific serum albumin are exemplary appropriate diluents.

One type of sustained release technology which may be used in administering soluble CD39 compositions is that utilizing hydrogel materials, for example, photopolymerizable hydrogels (Sawhney et al., *Macromolecules* 26:581; 1993). Similar hydrogels have been used to prevent postsurgical adhesion formation (Hill-West et al., *Obstet. Gynecol.* 83:59, 1994) and to prevent thrombosis and vessel narrowing following vascular injury (Hill-West et al., *Proc. Natl. Acad. Sci. USA* 91:5967, 1994). Polypeptides can be incorporated into such hydrogels to provide sustained, localized release of active agents (West and Hubbel, *Reactive Polymers* 25:139, 1995; Hill-West et al., *J. Surg. Res.* 58:759; 1995). The sustained, localized release of CD39 when incorporated into hydrogels would be amplified by the long half life of CD39, which is demonstrated in the Examples below.

Accordingly, the soluble CD39 compositions described herein can also be incorporated into hydrogels, for application to tissues for which localized inhibition of hemostasis is desirable. For example, a hydrogel incorporating a CD39 polypeptide can be applied to tissue after surgery, to prevent or reduce post-surgical adhesion formation, or can be applied using a catheter-based delivery system following angioplasty to prevent or reduce restenosis. Those of skill in the art will be able to formulate an appropriate hydrogel by applying standard pharmacokinetic studies, for example as discussed in West and Hubbell, *supra*.

Effective amounts may vary, depending on the age, type and severity of the condition to be treated, body weight, desired duration of treatment, method of administration, and other parameters.

Effective dosages are determined by a physician or other qualified medical professional. Typical dosages are 0.01-100 mg/kg body weight, preferably 0.1-10 mg/kg body weight. In some embodiments a single administration is sufficient; in some embodiments the soluble CD39 polypeptide is administered on a daily basis for up to a week or as much as a month or more.

The biological effectiveness of soluble CD39 polypeptides is easily evaluable: at given time intervals after administration, a prolongation of the bleeding time in the setting of unchanged platelet count should be measurable if released platelet ADP has been metabolized by the CD39 composition administered. This would indicate that a therapeutic effect has likely been obtained, as said measurement correlates with clinical improvement. A therapeutic effect can also be validated by testing platelet reactivity to ADP and other platelet agonists ex vivo. Actual measurements of enzyme (apyrase) activity can also be made following administration of soluble CD39. These and other methods of measuring biological effectiveness are illustrated in the Examples below.

H. Abbreviations Used in the Specification

ACR, apyrase conserved regions;
AG, Affigel beads;
ASA, acetylsalicylic acid;
ATPDase, ATP diphosphohydrolase;
CHO, Chinese hamster ovary;
CM, conditioned medium;
DHFR, dihydrofolate reductase;
FSBA, fluorosulfonylbenzoyl-adenosine;
HUVEC, human umbilical vein endothelial cells;
PRP, platelet-rich plasma;
PTCA, percutaneous transluminal coronary angioplasty;
solCD39, recombinant soluble human CD39;
TBS, Tris-buffered saline

EXAMPLES

The following examples are intended to illustrate particular embodiments and not to limit the scope of the invention.

EXAMPLE 1 **Assay For CD39 Expression**

This example describes the use of a monoclonal antibody in a FACS assay to analyze expression of CD39. The B73 mAb, a monoclonal anti-CD39, is a murine IgG1 that was derived from BALB/c mice immunized with the RPMI 1788 cell line (Rector et al., *Immunology* 55:481, 1985) and characterized as CD39-specific by flow cytometric analysis and immunoprecipitation/SDS-PAGE. Monoclonal anti-CD39 is purified from ascites fluid by affinity chromatography using a protein A column, eluted with 0.05 M sodium citrate, pH 3.0, neutralized and stored at 4°C at a concentration of about 1 mg/ml.

Cells to be analyzed (e.g., MP-1 cells, U937 cells, U937 cells stimulated with 5 ng/ml phorbol myristate acetate (PMA), or Daudi cells) are suspended to a concentration of 10^6 cell in 50 μ l of phosphate buffered saline (PBS) containing 100 μ g/ml human IgG1, and incubated for 30 minutes. The cells are then pelleted by centrifugation, resuspended in PBS/azide containing a first antibody (anti-CD39 or control antibody) and incubated (i.e., for 30 minutes at 4°C) The cells are then washed two times in PBS/azide, resuspended, and incubated with a labeled second antibody, for example, goat anti-murine immunoglobulin conjugated to phycoerythrin, then washed again. The cells are analyzed by flow cytometry, and levels of CD39 determined.

EXAMPLE 2

Immunoselection of Cells Expressing CD39

This example describes a panning (immunoselection) technique for cells expressing CD39. For the preparation of pan plates, purified anti-CD39 or control antibody is diluted in phosphate buffered saline containing 0.1% heat-inactivated fetal calf serum (PBS/FCS). A titration of anti-CD39 can be performed to determine the most effective concentration of anti-CD39. Pan plates are prepared by adding three ml of antibody solution or PBS/FCS alone to each plate. The plates are incubated for approximately one hour at room temperature, washed five times with PBS/FCS, and three ml of PBS/FCS containing 0.02% sodium azide are added to each plate.

The cells to be analyzed (e.g., MP-1, U937, or Daudi cells) are suspended in PBS/500 μ M EDTA/0.02% sodium azide (PEA) containing 5% goat serum, 5% rabbit serum and 100 μ g/ml human IgG1, to a concentration of 2×10^6 cells/ml; 500 μ l of each cell suspension is added to the prepared pan plates. The pan plates are incubated with the cell suspension for approximately two hours at room temperature, then the plates are washed gently three times with PEA containing 10% FCS (PEA/FCS), and three times with PEA. The plates are examined with a microscope, and the relative number of cells bound to each plate is determined.

EXAMPLE 3

cDNA Library Construction

This example describes preparation of a cDNA library from a human B cell line referred to as MP-1, for expression cloning of human CD39.

The library construction techniques were substantially similar to that described by Ausubel et al., eds., *Current Protocols In Molecular Biology*, Vol. 1, 1987. Briefly, total RNA was extracted from 8M guanidine HCl-lysed MP-1 cell cultures using differential ethanol precipitation and poly(A)⁺ mRNA was isolated and enriched by oligo dT cellulose chromatography. Double-stranded cDNA was made from an RNA template substantially as described by Gubler et al., *Gene* 25:263, 1983. Poly(A)⁺ mRNA fragments were converted to RNA-cDNA hybrids using reverse transcriptase primed with random hexanucleotides. The RNA-cDNA hybrids were then converted into double-

stranded cDNA fragments using RNAase H in combination with DNA polymerase I. The resulting double-stranded cDNA was blunt-ended with T4 DNA polymerase.

Unkinased (i.e. unphosphorylated) *Bgl*II adaptors were ligated to 5' ends of the above blunt-ended cDNA duplexes, using the adaptor cloning method described in Haymerle et al., *Nucleic Acids Res.* 14:8615, 1986. Under the described conditions, only the 24-mer oligonucleotide (top strand) will covalently bond to the cDNA during the ligation reaction. The non-covalently bound adaptors (including the complementary 20-mer oligonucleotide described above and any unligated adaptors) were removed by gel filtration chromatography at 65°C, leaving 24 nucleotide non-self-complementary overhangs on the cDNA termini.

The adapted cDNA was inserted into adapted pDC303, a mammalian expression vector that also replicates in *E. coli*. pDC303 was assembled from pDC201 (a derivative of pMLSV, previously described by Cosman et al., *Nature* 312: 768, 1984), SV40 and cytomegalovirus DNA and comprises, in sequence with the direction of transcription from the origin of replication, the following components: (1) SV40 sequences from coordinates 5171-270 containing the origin of replication, enhancer sequences and early and late promoters; (2) cytomegalovirus promoter and enhancer regions (nucleotides 671-63 from the sequence published by Boechar et al. (*Cell* 41:521, 1985); (3) adenovirus-2 from coordinates 5779-6079 containing the first exon of the tripartite leader (TPL), segment 7101-7172 and 9634-9693 containing the second exon and part of the third exon of the TPL and a multiple cloning site (MCS) containing sites for *Xho*I, *Kpn*I, *Sma*I and *Bgl*II; (4) SV40 segments from coordinates 4127-4100 and 2770-2533 containing the polyadenylation and termination signals for early transcription; (5) adenovirus-2 sequences from coordinates 10532-11156 of the virus-associated RNA genes VAI and VAII of pDC201; and (6) pBR322 sequences from coordinates 4363-2486 and 1094-375 containing the ampicillin resistance gene and origin of replication.

The MP-1 cDNA library in pDC303 was introduced into *E. coli* strain DH10B by electroporation. Recombinants were plated to provide approximately 5,000 colonies per plate. These recombinants were pooled to give a bulk stock of approximately 500,000 recombinants for screening. DNA was prepared from transformed bacteria and isolated by cesium chloride centrifugation.

EXAMPLE 4 Molecular Cloning of Human CD39 cDNA

This example describes the isolation of a DNA molecule encoding CD39 from the expression cloning library described in Example 3.

A. Round I: Transfection and Immunoselection

The isolated plasmid DNA was transfected into a sub-confluent layer of COS-7 cells using DEAE-dextran and a chloroquine treatment substantially according to the procedures described in McMahan et al., *EMBO J.* 10:2821; 1991.

COS-7 cells were maintained in transfection and growth medium (Dulbecco's modified Eagles' medium containing 10% (v/v) fetal calf serum, 50 U/ml penicillin, 50 µg/ml streptomycin, 2

mM L-glutamine and 50 µg/ml gentamicin) and were plated to a density of approximately 1.5×10^6 cells in 10 ml transfection and growth medium in 10 cm dishes. Medium was removed from adherent cells growing in a layer to approximately 70% confluency, and replaced with 10 ml complete medium containing 66.5 µM chloroquine. About 500 µl of a DNA solution (5 µg DNA, 0.5 mg/ml DEAE-dextran in transfection and growth medium containing 66.5 µM chloroquine) was added to the cells and the mixture was incubated at 37°C in 10 % CO₂ for about five hours.

Following incubation, media was removed and the cells were shocked by addition of 5 ml transfection and growth medium containing 10% DMSO (dimethylsulfoxide) for 2.5 - 20 minutes. Shocking was followed by replacement of the solution with 10 ml fresh transfection and growth medium. Twelve plates of cells were grown in culture for two to three days to permit transient expression of the inserted DNA sequences. The cells were trypsinized after about 24 hours of growth in order to remove them from the plates. After an additional one to two days, cells expressing CD39 were selected by panning, essentially as described in Example 2. The cells were incubated in the mAb 73 pan plates for two hours at room temperature, after which unbound cells were removed by gently rinsing three times with PEA/FCS, then three times with PEA.

The cells that were not removed by rinsing were expressing CD39; cells expressing CD39 were lysed by the addition of 700 µl lysing buffer containing sodium dodecyl sulfate (SDS) and incubation for 20 minutes at room temperature. Lysates were transferred from each dish to individual microfuge tubes containing 100 µl of 5 M NaCl. The tubes were capped, mixed thoroughly by inverting about 20 times, and stored at 4°C overnight. After overnight incubation at 4°C, high molecular weight DNA (debris) was removed by centrifugation, and 2 µg of glycogen was added to each supernatant. The supernatants were then extracted twice with phenol/chloroform and once with chloroform/isoamyl alcohol. DNA was ethanol precipitated, washed with 80% ethanol, and vacuum dried. The purified DNA was then electroporated into *E. coli*, which were then plated out on ampicillin plates. A large-scale transformation was carried out in this manner, yielding a total of approximately 48,000 colonies (sub-library 1). DNA was prepared from the colonies using CsCl; frozen stocks of the colonies were prepared at the same time.

B. Round II: Electroporation and Immunoselection

The DNA from sub-library 1 was electroporated into COS cells (10 x 10 cm plates). Transfected COS cells were incubated, harvested and panned substantially as described for Round I above. DNA was isolated and a sub-library (sub-library 2) of approximately 50,000 independent colonies was prepared substantially as described above.

C. Round III: Electroporation and FACS Selection

The DNA from sub-library 2 was electroporated into COS cells (10 x 10 cm plates). Transfected COS cells were incubated and harvested substantially as described for Round I above. The harvested cells were analyzed by FACS substantially as described in Example 1 above. A small subpopulation of cells expressing CD39 was observed, and was sorted out from the larger mixture of

cells; DNA was isolated from the sorted cells. A sub-library (sub-library 3) of approximately 5,000 independent colonies was prepared. The DNA was pooled into 10 pools of approximately 500 colonies each; isolated DNA and frozen stocks of bacteria were prepared for each pool.

D. Round IV: Transfection and Immunoselection

5 The DNA from sub-library 3 was transfected into COS cells using DEAE-dextran and chloroquine treatment, and incubated, substantially as described for Round I above, except that the cells were incubated on fibronectin-treated, chambered slides (10 slides, 1 for each pool, and 4 control slides) instead of 10 cm plates. After two days of growth, the cells were harvested as described, and analyzed by FACS substantially as described in Example 1 above, as well as by a slide dipping
10 technique. In the slide dipping technique, the slides were incubated with ¹²⁵I-labeled mAb 73 and fixed with glutaraldehyde. The results were determined by autoradiography using light microscopy to detect cell containing silver granules.

Two pools containing approximately 500 individual clones each were identified as potentially positive for production of CD39. The pools were titered and plated to provide plates containing an
15 average of approximately 150 colonies each. A replicate nitrocellulose filter was prepared from each plate; each plate was then scraped to provide smaller pools of plasmid DNA.

E. Round V: Transfection and Immunoselection

COS-7 cells were transfected with the DNA from the smaller pools by DEAE-dextran, according to the same procedure described above. The transfected cells were screened by slide
20 dipping and FACS as described previously. Two of the smaller pools contained clones that were positive for CD39 as indicated by the presence of an expressed gene product that bound mAb 73.

A total of 156 colonies was picked from the replicate filter corresponding to one of the positive smaller pools, and inoculated into culture medium for overnight growth. After overnight growth, the cultures were arranged in a matrix format of 12 rows and 13 columns. Subpools of culture
25 medium were prepared by pooling medium from each row and each column for a total of 24 subpools. The subpools were used to prepare DNA for a final round of transfection and screening. An intersection of a positive row and a positive column indicated a potential positive colony. One potential positive colony (i.e. clone) was identified.

A streak plate was prepared from the positive clone (clone 1), and minipreps of DNA were
30 made from nine individual colonies from the streak plate. The DNA was digested with Bgl II and analyzed by SDS-PAGE. Nine of nine individual colonies from clone 1 contained identical inserts of 1.8 - 2.0 Kb. A single isolate that contained the 1.8 - 2.0 Kb insert was picked and inoculated into 10 ml culture medium for overnight growth. DNA was prepared and sequenced by dideoxynucleotide sequencing. The nucleotide and deduced amino acid sequence of clone 1 is given in SEQ ID NO:1. A
35 cloning vector containing human CD39 sequence, designated pCD39 was deposited with the American Type Culture Collection, Rockville, MD (ATCC) on September 29, 1992, under the Budapest Treaty, and assigned accession number 69077. A murine homolog of CD39 was isolated by

cross-species hybridization; the amino acid sequence of the murine homolog is described in Maliszewski et al., *J. Immunol.* 153:3574, 1994.

EXAMPLE 5 Preparation of CD39 mAbs

This example describes the preparation of additional monoclonal antibodies against CD39, including antibodies against the region that contains apyrase activity. Preparations of purified CD39 fragments exhibiting ADPase activity, for example, or transfected cells expressing such CD39 polypeptides, are employed as immunogens to generate monoclonal antibodies against CD39 using conventional techniques, such as those disclosed in U.S. Patent 4,411,993. DNA encoding CD39 fragments can also be used as an immunogen, for example, as reviewed by Pardoll and Beckerleg in *Immunity* 3:165, 1995. Such antibodies are useful for interfering with CD39-induced platelet aggregation, as components of diagnostic or research assays for CD39 or CD39 activity, and in affinity purification of CD39.

To immunize rodents, CD39 immunogen is emulsified in an adjuvant (such as complete or incomplete Freund's adjuvant, alum, or another adjuvant, such as Ribi adjuvant R700 (Ribi, Hamilton, MT), and injected in amounts ranging from 10-100 µg subcutaneously into a selected rodent, for example, BALB/c mice or Lewis rats. DNA may be given intradermally (Raz et al., *Proc. Natl. Acad. Sci. USA* 91:9519, 1994) or intramuscularly (Wang et al., *Proc. Natl. Acad. Sci. USA* 90:4156, 1993); saline has been found to be a suitable diluent for DNA-based antigens. Ten days to three weeks days later, the immunized animals are boosted with additional immunogen and periodically boosted thereafter on a weekly, biweekly or every third week immunization schedule.

Serum samples are periodically taken by retro-orbital bleeding or tail-tip excision for testing by dot-blot assay (antibody sandwich), ELISA (enzyme-linked immunosorbent assay), immunoprecipitation, or other suitable assays, including FACS analysis. Following detection of an appropriate antibody titer, positive animals are given an intravenous injection of antigen in saline. Three to four days later, the animals are sacrificed, splenocytes harvested, and fused to a murine myeloma cell line (e.g., NS1 or preferably Ag 8.653 [ATCC CRL 1580]). Hybridoma cell lines generated by this procedure are plated in multiple microtiter plates in a selective medium (for example, one containing hypoxanthine, aminopterin, and thymidine, or HAT) to inhibit proliferation of non-fused cells, myeloma-myeloma hybrids, and splenocyte-splenocyte hybrids.

Hybridoma clones thus generated can be screened by ELISA for reactivity with CD39, for example, by adaptations of the techniques disclosed by Engvall et al., *Immunochem.* 8:871, 1971 and in U.S. Patent 4,703,004. A preferred screening technique is the antibody capture technique described by Beckman et al., *J. Immunol.* 144:4212, 1990. Positive clones are then injected into the peritoneal cavities of syngeneic rodents to produce ascites containing high concentrations (>1 mg/ml) of anti-CD39 monoclonal antibody. The resulting monoclonal antibody can be purified by ammonium sulfate precipitation followed by gel exclusion chromatography. Alternatively, affinity chromatography based

upon binding of antibody to protein A or protein G can also be used, as can affinity chromatography based upon binding to CD39 polypeptide. An alternative strategy is to employ full-length CD39 immunogen, selecting for antibodies that bind CD39, and winnowing out those that bind to previously defined epitopes, for example by screening with a fragment of CD39 that represents a previously defined epitope.

Monoclonal antibodies are also prepared by immunizing CD39 knockout mice, such as those described in Example 19D, with CD39 immunogen. Since the entire CD39 sequence is seen as "foreign" in the knockout mice, this strategy can lead to the generation of antibodies recognizing epitopes that are shared across species lines, including antibodies that antagonize or agonize CD39 bioactivity.

EXAMPLE 6 Physiological Activity of CD39

This example demonstrates that CD39 is the endothelial cell ecto-ADPase responsible for inhibition of platelet function. Human umbilical vein endothelial cells (HUVEC) constitutively inhibit platelet responsiveness to prothrombotic stimuli by catabolism of exogenous platelet-derived ADP. The endothelial ecto-ADPase has been identified as CD39 (Marcus et al., *J. Clin. Invest.* 99:1351, 1997). Anti-CD39 antibodies immunoprecipitated ADPase activity from a preparation derived from endothelial membranes, and COS cells transfected with an expression vector comprising CD39 acquired ecto-ADPase activity whereas COS cells transfected with a control vector did not. Ecto-ADPase activity was measured in a manner similar to that described in Marcus et al., *J. Clin. Investigation* 88:1690, 1991, by conversion of ¹⁴C-ADP to AMP by transfectant monolayers as well as membrane preparations, and was greater than or comparable to activity of intact HUVEC monolayers and solubilized membranes

HUVEC mRNA was analyzed by RT-PCR using primer pairs derived from the sequence of the human CD39 lymphoid cell activation antigen with emphasis on its N-terminal portion. Lymphoid CD39 cDNA was used for direct comparison of PCR product sizes. The data demonstrated identity between HUVEC and lymphoid CD39 in the 4 fragments spanning the portion analyzed (approximately 1250 of the 1850 bp of lymphoid CD39). Northern blot analyses revealed that the mRNA for CD39 in HUVEC was expressed in the same band pattern as in MP-1 cells, from which CD39 was originally cloned.

Confocal microscopy and fluorescence activated cell sorting, using mAb73, were used to determine if HUVEC cells expressed CD39. The FACS protocol was substantially as described in Example 1. For confocal microscopy, cells (human umbilical vein endothelial or transfected COS-1 cells) grown on coverslip glass were washed with PBS and fixed with 3% paraformaldehyde for 30 minutes at room temperature. Auto fluorescence was quenched by treatment with 50mM NH₄Cl for 10 minutes. Cells were then incubated in PBS containing 5% NGS (normal goat serum) plus 0.1% triton X-100 to block non-specific binding and to permeabilize cells. Cells were then incubated with

anti-CD39 antibody at 5 µg/ml in PBS containing 5% NGS +0.1% triton X-100 for 1 hour at room temperature. Following three washes with PBS containing 5% NGS +0.1% triton X-100 cells were incubated with goat anti-mouse labeled with Texas Red (Molecular Probes) at 5 µg/ml in addition to 10 mM YOYO (Molecular Probes) for nucleic acid counter stain, for 1 hour at room temperature.

5 Cells were washed 3 times with PBS containing 5% NGS +0.1% triton X-100 and mounted in 100 mg/ml DABCO (1,4 diaxabicyclo [2.2.2] octane) (Sigma) in 50% glycerol. Cells were then viewed with Multiprobe 2001 laser scanning confocal microscope (Molecular Dynamics). One image was collected of CD39 staining (Texas Red) and a second image was collected of cell nuclei (YOYO).

Both the confocal microscopy and FACS experiments demonstrated that HUVEC express
10 CD39. The patterns of expression were similar to those seen in cells transfected with full-length human CD39.

The physiological activity of CD39 was illustrated by the ability of CD39-transfected COS cells to inhibit and completely reverse platelet aggregation by 10 µM ADP. CD39-transfected COS cells, as well as MP-1 cells and HUVEC, metabolized this quantity of ADP to AMP within three to
15 four minutes and, when added to platelet rich plasma (substantially as described in Marcus et al., *supra*), they rapidly reversed platelet aggregation. This activity occurred within the time frame of platelet adhesion to injured subendothelium, a process leading to immediate ADP release, recruitment of additional platelets and formation of a hemostatic plug or thrombus. This time course paralleled platelet inhibition by CD39-expressing cells, and was commensurate with their ADPase activities.
20 The activity of ADPase/CD39 was independent of formation of other known thromboregulators, nitric acid or prostacyclin. These results demonstrate the importance of ADPase/CD39 as a physiological, constitutively expressed endothelial cell thromboregulator.

EXAMPLE 7

Phosphate Release Assay for ATPase Activity

This example describes an ATPase assay that may be used to track enzyme activity. Samples (approximately 100 µl of either concentrated CM or purified polypeptide) are combined with 20 µl of 10X assay buffer (200 mM HEPES, 1.2 M NaCl, 50 mM KCl, 15 mM CaCl₂, 15 mM MgCl₂ and 3 mM ATP) and sterile water is added to a final volume of 200 µl. Radiolabeled ATP (0.8 µCi γ [³²P]
30 ATP; Amersham, Arlington Heights, IL) is added and the mixture incubated for 20 minutes at 37°C. Stop mix (0.5 ml of 20% activated charcoal/1 M HCl) is added and the reaction is placed on ice for 10 minutes. After centrifugation (14K rpm for 10 minutes), the supernatant is assayed for free ³²P using a scintillation counter. Data are expressed as raw counts or net counts, or as picomoles of ATP degraded per minute.

EXAMPLE 8

Binding Assay

This example describes an assay to assess the binding of CD39 polypeptides to CD39 antibodies by biospecific interaction analysis (BIA) using a biosensor, an instrument that combines a

biological recognition mechanism with a sensing device or transducer. An exemplary biosensor is BIAcoreTM, from Pharmacia Biosensor AB (Uppsala, Sweden; see Fägerstam L.G., *Techniques in Protein Chemistry II*, ed. J.J. Villafranca, Acad. Press, NY, 1991). BIAcoreTM uses the optical phenomenon surface plasmon resonance (Kretschmann and Raether, *Z. Naturforschung, Teil. A* 23:2135, 1968) to monitor the interaction of two biological molecules. Molecule pairs having affinity constants in the range 10^5 to 10^{10} M⁻¹, and association rate constants in the range of 10^3 to 10^6 M⁻¹s⁻¹, are suitable for characterization with BIAcoreTM.

The biosensor chips are coated with CD39 antibody (e.g., mAb73). The different constructs of CD39 to be assessed are then added at increasing concentrations; the chip is regenerated between the different constructs, for example, by the addition of sodium hydroxide. The resultant data can be analyzed to qualitatively or quantitatively assess production of CD39 polypeptides. Affinity of the CD39 polypeptides for the CD39 antibodies can also be determined. In a similar manner, other monoclonal antibodies or polypeptides that specifically bind CD39 can be immobilized on a biosensor chip to assess the binding of various CD39 polypeptides.

EXAMPLE 9

Transient Expression of Soluble CD39 Polypeptides

This example describes the preparation of constructs for the transient expression of soluble CD39 polypeptides.

A. Reagents Used

The B73 mAb, a murine IgG1 recognizing human CD39, was kindly provided by Dr. Guy Delespesse (U. Montreal, Quebec, Canada). The M2 mAb recognizing the FLAG[®] peptide (DYKDDDDK, SEQ ID NO:10), a murine IgG1, was prepared at Immunex Corp. Affigel 10 (Bio-Rad, Hercules, CA) and CNBr-activated Sepharose 4B (Pharmacia Biotech, Piscataway, NJ) immunoaffinity columns were prepared according to manufacturers' instructions. Typically, coupling efficiencies in the range of 3-5 mg mAb per ml of affinity gel slurry were obtained.

B. Construction of a Soluble CD39 (solCD39) Expression Plasmid

To generate a soluble molecule having the properties of CD39 the N-terminal and C-terminal portions of CD39, including the two transmembrane regions (see Fig. 2), were removed. To allow transport of soluble CD39 into the medium, a leader sequence providing for secretion was added at the amino terminus of the polypeptide.

Constructs of soluble human CD39 (solCD39) were made in the mammalian expression vector pDC206 (Kozlosky et al. *Oncogene*. 10:299, 1995), utilizing human IL2 (huIL2), human growth hormone (huGH) and murine IL7 (muIL7) leaders).

The DNA sequences between the putative transmembrane regions of full-length CD39, including nucleotides 178-1494 of SEQ ID NO:1, were amplified using PCR and the C-terminal transmembrane coding region was replaced with a stop codon. The PCR product was fused to a synthetic DNA fragment encoding an 8 amino acid peptide tag (FLAG[®]) and ligated with a muIL7 leader (muIL7L) into the plasmid pDC206 vector via SpeI and BglII restriction sites. This construct encoded N-terminally FLAG-tagged solCD39.

Alternate leaders were introduced by ligating the SpeI/BglII FLAG-solCD39 fragment into two different pDC206 plasmids, with leaders derived from: (1) human growth hormone (huGHL), and (2) a human proinsulin/IL2 fusion polypeptide (huIL2L, Cullen, *DNA*. 7:645, 1988). The coding region of the latter construct, which is shown in SEQ ID NOs:25 and 26, includes sequences encoding the huIL2 leader (huIL2L, nucleotides 1-72, amino acids 1-24 in SEQ ID NO:25), the first 12 amino acids of mature human IL2 (nucleotides 73-108, amino acids 25-36 in SEQ ID NO:25), a four amino acid linker (nucleotides 109-120, amino acids 37-40 in SEQ ID NO:25), the FLAG tag (nucleotides 121-144, amino acids 41-48 of SEQ ID NO:25), and sol CD39 (nucleotides 145-1461, amino acids 49-487 of SEQ ID NO:25).

The constructs comprising the muIL7 leader, the human growth hormone leader, and the human proinsulin/IL2 leader were designated pIL7LFlagSolCD39, pGHLFlagSolCD39, and pIL2LFlagSolCD39 respectively.

Each construct was used to transiently transfect subconfluent layers of COS-1 cells using DEAE dextran followed by chloroquine as described by Cosman et al., *Nature* 312:768, 1984. As a negative control, a CD40 ligand construct (pIL2LCD40lig, Spriggs et al., *J. Exp. Med.* 176:1543, 1992) was also transfected into COS-1 cells.

C. Preparation of Conditioned Medium from solCD39 Transfectants

The transfected COS-1 cells were incubated (37°C, 5% CO₂) in 0.5% FCS-supplemented DMEM-F12 medium in 10 cm² Petri dishes or 175 cm² tissue culture flasks. After 5 days, conditioned medium (CM) from these cultures was collected, and cells and debris were removed by centrifugation. The CM was concentrated 4-10 fold using a pressurized, stirred cell fitted with a YM-10 (10 kD cutoff) membrane (Amicon Corp., Danvers, MA).

D. ATPase Activity in Conditioned Medium from solCD39 Transfectants

ATPase activity in the CM from solCD39 transfectants (100 µL of 10-fold concentrated supernatant) was assayed essentially as described in Example 7, except that the 10X assay buffer contained 30 mM cold ATP. The results are shown in TABLE 1.

The transfections were repeated and the CM (10, 20 and 30 µL, unconcentrated) was assayed essentially as described in Example 7. The results are shown in TABLE 2. Because the pIL2LFlagSolCD39 showed higher ATPase activity in COS-1 supernatants than pIL7LFlagSolCD39 and pGHLFlagSolCD39, this construct was selected for further investigation. ATPase levels in CM

from COS-1 cells transfected with pIL2LFlagSolCD39 increased with time in culture over at least 4 days post-transfection.

TABLE 1
ATPase Activity in Concentrated CM from solCD39 Transfectants

Sample	CPM Release x 10 ³ (raw counts)
pIL2LFlagSolCD39	99.96
pIL7LFlagSolCD39	39.47
pGHLFlagSolCD39	21.14
pIL2LCD40lig	10.53
media only	7.89

TABLE 2
ATPase Activity in CM from solCD39 Transfectants

Sample	Vol (μL)	CPM Release x 10 ³ (net counts)
pIL2LFlagSolCD39	10	24.71
	20	43.92
	30	56.93
pIL7LFlagSolCD39	10	5.01
	20	9.75
	30	14.23
pGHLFlagSolCD39	10	5.51
	20	7.22
	30	9.95

10 E. Immunoaffinity Depletion of solCD39 from COS-1 CM

To confirm that recombinant solCD39 accounted for the ATPase activity observed in the CM, CM from COS-1 transfectants was incubated with immunoaffinity beads prior to enzyme assay.

CM was collected from COS-1 cells transfected with pIL2LFlagSolCD39, which had been cultured for 5 days in DMEM/F12 supplemented with 5% FCS. A 100 μl aliquot of drained Affigel beads (AG) conjugated with either chicken ovalbumin, antiFLAG mAb, or anti-CD39 mAb was added per ml of CM. CM was subjected to one or two cycles of binding with one of the following: ovalbumin-conjugated AG, M2 mAb-conjugated AG, or B73 mAb-conjugated AG. Each cycle involved continuous gentle agitation of the slurry for 14 h at 4°C followed by centrifugation to recover supernatants for a subsequent binding cycle or for ATPDase activity measurements.

20 As shown in Fig. 3, immunoprecipitation with anti-CD39 mAb-conjugated beads resulted in removal of over 80% of ATPase activity from CM. Over 95% ATPase activity was removed with a second antibody adsorption step. Immunoprecipitation (2 cycles) with anti-FLAG mAb-coated beads also resulted in substantial depletion of enzyme activity. Two rounds of preincubation with a control (ovalbumin-conjugated beads) did not remove significant ATPase activity from the supernatants.

F. Immunoprecipitation of Recombinant solCD39

To characterize recombinant solCD39 polypeptide expression, COS-1 cells were transfected with mammalian expression vectors encoding cell surface CD39 (pHuCD39, Marcus et al., *J. Clin. Invest.* 99:1351, 1997), tagged soluble CD39 (pIL2LFlagSolCD39), or soluble CD40 ligand (pIL-2L-CD40L) and grown in 5% FCS-supplemented DMEM/F12 medium in 10 cm² dishes. Two days after transfection, the medium was replaced with Cys/Met-free medium and cells were incubated for 1 h at 37°C. The culture medium was replaced with fresh Cys/Met-free medium supplemented with 5 µl of [³⁵S]-Cys/Met (Amersham, Arlington Heights, IL) in order to label newly synthesized polypeptides, and cells were cultured for 5 h at 37°C. CM from the metabolically radiolabeled cells was collected, purified of cells and debris by centrifugation and sterile filtration, and stored at 4°C until further use.

For radioimmunoprecipitation, 500 µl of ³⁵S-labeled CM was added to 250 µl of 3% BSA in Tris-buffered saline (TBS), pH 7.7, followed by addition of 50 µl of a 80% slurry of mAb-coated AG beads. In some cases, ³⁵S-labeled CM were incubated with ovalbumin-coated AG beads to remove nonspecifically binding materials prior to addition of Ab-coated beads. After incubation for 14 h at 4°C, beads were removed by centrifugation and washed three times in cold TBS.

For SDS-PAGE analysis, 35 µl of 4-fold concentrated reducing sample buffer (250 mM Tris/HCl, pH 6.8, 8 % (w/v) SDS, 40 % (v/v) glycerol, 20% (v/v) 2-mercaptoethanol, 0.05% bromophenol blue dye) was added to each AG pellet, boiled for 5 min, and loaded onto a 8-16% Novex (San Diego, CA) polyacrylamide gel. Gels were electrophoresed at 25 mA, prepared for autoradiography by soaking in Enhance (NEN Life Science Products, Boston, MA) for 1 h and in H₂O for 20 min, followed by vacuum drying at 80°C. Gels were exposed to Kodak (Rochester, NY) X-omat AR film for 2 h, then developed.

As shown in Fig. 4, IL-2L-FlagsolCD39 transfectants secreted a radiolabeled protein of ~66 kD that was recognized by anti-CD39. This protein was not detected in anti-CD39 immunoprecipitated CM from COS-1 cells transfected with a vector encoding full-length CD39 (including N-terminal and C-terminal hydrophobic regions), or with a vector encoding a secreted protein, CD40 ligand. Anti-FLAG mAb immunoprecipitated a similar-sized band from CM of the pIL-2L FlagsolCD39 transfectant, consistent with the presence of the FLAG[®] peptide in recombinant solCD39. Preclearing radiolabeled culture supernatants with anti-ovalbumin-coated beads failed to remove the 66 kD band, indicating that binding to anti-CD39 and anti-FLAG was specific. Beads coated with an irrelevant, isotype matched control antibody failed to immunoprecipitate the 66 kD band from solCD39 containing CM.

G. Preparation of Additional solCD39 Fusion Constructs

Restriction enzymes were used to prepare a DNA fragment comprising nucleotides 1 through 1488 of SEQ ID NO:1, the coding region of which would be expected to encode a fragment of CD39 lacking the second (most C-terminal) transmembrane domain. Appropriate linker oligonucleotides

were prepared (SEQ ID NOs:14 and 15), and used in a three-way ligation of the CD39 DNA, the linker oligonucleotides, and an expression vector comprising regulatory elements allowing expression of a resulting fusion polypeptide in mammalian cells along with DNA encoding a mutated human immunoglobulin Fc (SEQ ID NOs:16 and 17) region that exhibits reduced affinity for Fc receptors (nucleotides 42 through 740 of SEQ ID NO:16). This construct was referred to as CD39Δ2Fc, and when transfected into cells resulted in the expression of a fusion polypeptide comprising amino acids 1 through 474 of SEQ ID NO:1 and amino acids 1 through 232 of SEQ ID NO:17, which could be detected on the surface of transfected cells using either anti-CD39 or anti-human IgG.

A PCR technique was employed to prepare a fragment of DNA from the CD39Δ2Fc construct that also lacked the first, most amino-proximal transmembrane region, but included CD39 DNA from nucleotides 181 through 1488 (amino acids 39 through 474) of SEQ ID NO:1 and the Fc mutein DNA from CD39Δ2Fc (using the linkers shown in SEQ ID NOs:18 and 19).

The resulting DNA was then ligated into an expression vector that included DNA encoding the murine Interleukin-7 leader sequence (SEQ ID NO:20) ligated immediately proximal to the CD39-encoding sequence. This construct was designated CD39Δ1,Δ2Fc.

DNA encoding the FLAG[®] peptide (SEQ ID NO:10) and a codon corresponding to nucleotides 178, 179 and 180 of SEQ ID NO:1 was inserted into the CD39Δ1,Δ2Fc construct, in between the leader sequence and the CD39-encoding sequence, to provide a detectable tag for the amino terminus of the fusion polypeptide (using the linkers shown in SEQ ID Nos:21 and 22). The tagged construct was referred to as FlagCD39Δ1,Δ2Fc.

Another construct was prepared that removed the Fc mutein sequences, and added codons corresponding to nucleotides 1489 through 1494 of SEQ ID NO:1 immediately downstream of the CD39 sequences (using the linkers shown in SEQ ID Nos:23 and 24). This construct was designated FlagCD39Δ1,Δ2.

Each of the constructs was transfected into mammalian cells and protein levels were assayed on the surface, in the interior, or in the supernatant fluid of transfected cells using antibodies to FLAG[®], CD39, or human IgG.

EXAMPLE 10 **Expression and Activity of pIL2LSolCD39**

To facilitate the establishment of a stably producing transfectant in CHO cells, an untagged version of soluble human CD39 (solCD39) was constructed. A 523 bp Spe1/Nde1 fragment containing the FLAG[®] tag and the first 163 amino acids (aa) of pIL2LFlagSolCD39 was removed, and replaced with a similar fragment from a C-terminally FLAG[®]-tagged solCD39. Thus the entire solCD39 coding region was reconstituted, sans FLAG[®], while retaining the HuIL2 leader and mature IL2 residues. This construct was designated pIL2LSolCD39. The coding region of pIL2LSolCD39,

which is shown in SEQ ID NO:7, includes sequences encoding the huIL2 leader (huIL2L, nucleotides 1-72, amino acids 1-24 in SEQ ID NO:7), the first 12 amino acids of mature human IL2 (nucleotides 73-108, amino acids 25-36 in SEQ ID NO:7), a three amino acid linker (nucleotides 109-117, amino acids 37-39 in SEQ ID NO:7), and sol CD39 (nucleotides 118-1434, amino acids 40-478 of SEQ ID NO:7).

To determine whether activity was affected by removal of the N-terminal FLAG[®] tag, COS-1 cells were transfected with pIL2LFlagSolCD39 and pIL2LSolCD39 and supernatants (sups) were harvested after 5 days. Samples of 10, 20 and 30 μ L of 1x sups were assayed for ATPase activity as described in Example 7. As shown in TABLE 3, activity was not affected by removal of the N-terminal FLAG[®] tag.

TABLE 3
ATPase Activity in CM from pIL2LFlagSolCD39 and pIL2LSolCD39 Transfectants

Sample	Vol (μ L)	CPM x 10 ³ (net counts)
pIL2LFlagSolCD39	10	23.6
	20	40.2
	30	54.4
pIL2LSolCD39	10	20.1
	20	36.0
	30	51.0

EXAMPLE 11

Preparation of Additional solCD39 Fusion Constructs

A. Preparation and Characterization of Trim1 and Trim2 Variants

To characterize the effect of the 12 mature human IL2 (huIL2) residues on the expression of solCD39, the huIL2 residues were removed during the construction of nucleic acid sequences encoding two additional variants of pIL2LSolCD39: pIL2LTrim1 ("Trim1") and pIL2LTrim2 ("Trim2").

The pIL2LTrim1 variant was constructed by purifying a Hind3/Bgl2 restriction fragment from pIL2LSolCD39 which contained the entire solCD39 coding region except for the first four amino acids. This fragment was ligated with a synthetic oligo cassette (containing the huIL2 leader and the first amino acid of mature huIL2) into Sma1/Bgl2 digested pDC206. The huIL2 leader was thus reintroduced and joined to solCD39 with an intervening alanine residue.

The pIL2LTrim2 variant was constructed in a similar fashion using a Spe1/Bgl2 fragment from pIL2LSolCD39 and a synthetic oligo cassette containing the huIL2 leader and the linker-encoded sequences (with the first codon altered to alanine). Thus, the huIL2 leader was restored with an intervening Ala-Ser-Ser linker preceding solCD39.

The N-terminal portions of the pIL2LSolCD39, pIL2LTrim1 and pIL2LTrim2 polypeptides are compared below, with the predicted cleavage points indicated as *:

pIL2LSolCD39 (SEQ ID NO:11)

MALWIDRMQLLSCIALSLALVTNS*APTSSSTKKTQLts sT QNK...

pIL2LTrim1 (SEQ ID NO:12)

MALWIDRMQLLSCIALSLALVTNS A T*QNK...

pIL2LTrim2 (SEQ ID NO:13)

MALWIDRMQLLSCIALSLALVTNS as*sT QNK...

The polypeptide encoded by the Trim1 construct has the sequence SEQ ID NO:27. Residues 26-464 are a soluble portion of CD39 and the cleavage of the leader sequence is between Ser24 and Ala25.

The expression of Trim1 and Trim2 constructs was analyzed in COS-1 cells cultured in 10 cm plates. After 5 days of incubation, 1x supernatants were examined via ELISA (using anti-CD39) and the phosphate-release assay described in Example 7. As shown in TABLE 4, the specific activities (based on concentrations determined by ELISA) of Trim1 and Trim2 were equivalent to pIL2LFlagSolCD39. Expression levels, however, appeared to be reduced 3-4 fold.

TABLE 4
SolCD39 Expression and Activity in CM from pIL2LSolCD39 an Trim Transfectants

Sample	[CD39] $\mu\text{g/mL}$	Activity (pmol ATP/min/ μg) $\times 10^3$
pIL2LSolCD39	0.75	5.67
pIL2LTrim1	0.21	8.38
pIL2LTrim2	0.21	6.67

COS-1 cells were also transfected with pIL2LSolCD39, pIL2LTrim1 and pIL2LTrim2 and cultured in T175 flasks (30 mL). 5-day/1x sups were then analyzed via ELISA. As shown in TABLE 5, the ELISA results again indicated lower expression levels for the Trim1 and Trim2 variants.

To further characterize the effect of the human IL2 (huIL2) residues on the expression of solCD39, the pIL2LSolCD39, pIL2LTrim1, and pIL2LTrim2 products were purified using anti-CD39 coated sepharose. The N-terminal amino acid sequence was determined for each of the purified polypeptides. For solCD39 the N-terminus was APTSSSTKKT. . . (residues 25-34 of SEQ ID NO:11). For Trim1 the N-terminus was ATQNKALPEN. . . (residues 25-34 of SEQ ID NO:27). The Trim2 polypeptides had heterogeneous N-termini.

TABLE 5
SolCD39 Expression in CM from pIL2LSolCD39 and Trim Transfectants

Sample	[CD39] $\mu\text{g/mL}$
pIL2LSolCD39	0.796
pIL2LTrim1	0.143
pIL2LTrim2	0.113

B. Preparation and Characterization of Trim3 and Trim4 Variants

Nucleic acids encoding additional solCD39 variants, designated pIL2LTrim3 ("Trim3") and pIL2LTrim4 ("Trim4"), are also constructed using a synthetic oligo cassette strategy. The N-terminal portions of the solCD39, Trim3 and Trim4 polypeptides are compared below. The predicted cleavage points are indicated as *.

pIL2LSolCD39 MALWIDRMQLLSICIALSLALVTNS*APTSSST KKTQLtssTQNK...
(SEQ ID NO:11)

pIL2LTrim3 MALWIDRMQLLSICIALSLALVTNS*A ST KKTQLtssTQNK...
(SEQ ID NO:28)

pIL2LTrim4 MALWIDRMQLLSICIALSLALVTNS ST*KKTQLtssTQNK...
(SEQ ID NO:29)

The polypeptide encoded by the Trim3 construct has the sequence SEQ ID NO:28. Residues 36-474 are a soluble portion of CD39 and the predicted cleavage of the leader sequence is between Ser24 and Ala25. The polypeptide encoded by the Trim4 construct has the sequence SEQ ID NO:29. Residues 35-473 are a soluble portion of CD39 and the predicted cleavage of the leader sequence is between Thr26 and Lys27.

The pIL2LTrim3, and pIL2LTrim4 polypeptides are expressed and purified using anti-CD39 coated sepharose. The N-terminal amino acid sequence and specific activity are determined for each of the polypeptides.

C. Preparation and Characterization of solCD39-L4 Fusion Polypeptides

The CD39 gene family is reported to contain at least four human members: CD39, CD39L2, CD39L3, and CD39L4 (Chadwick and Frischauf, *Genomics* 50:357, 1998). CD39-L4 is reported to be a secreted apyrase (Mulero et al., *J. Biol. Chem.* 274(29):20064, 1999). Additional solCD39 variants are constructed by fusing N-terminal sequences from CD39L2, CD39L3, or CD39L4 to a soluble portion of CD39. The N-terminal amino acid sequences of human CD39 and human CD39-L4 are aligned in Fig. 24.

For one construct, CD39-L4-1, a nucleic acid encoding CD39-L4 amino acid residues 1-37 (Met1 to Ser37 of SEQ ID NO:31) is fused to a nucleic acid encoding CD39 residues 38-476 (Thr38 to Thr476 of SEQ ID NO:2). The polypeptide encoded by the CD39-L4-1 construct has the sequence SEQ ID NO:3. Residues 1-37 are from CD39-L4, residues 38-476 are a soluble portion of CD39, and the predicted site of cleavage of the leader sequence is between Ala20 and Val21.

For another construct, CD39-L4-2, a nucleic acid encoding CD39-L4 amino acid residues 1-48 (Met1 to Leu48 of SEQ ID NO:31) is fused to a nucleic acid encoding CD39 residues 49-476 (Tyr49 to Thr476 of SEQ ID NO:2). Another construct, CD39-L4-3, is identical to CD39-L4-2 except that the Cys residue at position 39 (Cys39) is replaced by another amino acid, preferably Ser. The polypeptides encoded by the CD39-L4-2 and CD39-L4-3 constructs have the sequence SEQ ID NO:4.

Residues 1-48 are from CD39-L4, residues 49-476 are a soluble portion of CD39, and the predicted site of cleavage of the leader sequence is between Ala20 and Val21.

Additional constructs are constructed by fusing a portion of the CD39-L4 N-terminal coding region to the CD39 N-terminal coding region. After expression in recombinant cells, the N-terminal sequence, enzymatic activity, and platelet inhibitory activity is determined for each of the polypeptide products.

D. Preparation and Characterization of IgkappaLsolCD39

Nucleic acids encoding an Igkappa leader sequence fused to amino acids from IL-2 and to solCD39 are also constructed. One such construct encodes a polypeptide having an Igkappa leader and four amino acids from IL-2 fused to the N-terminus of the CD39 soluble portion (set forth as residues Thr38 to Thr476 of SEQ ID NO:2). The N-terminus of the encoded polypeptide is therefore: 5'-METDTLLLWVLLLWVPGSTG*APTSTQNKALPE . . . (amino acids 1-32 of SEQ ID NO:30), where amino acids Met1-Gly20 are the Igkappa leader, Ala21-Ser24 are from IL-2, and Thr25-Glu32 is the beginning of solCD39 sequences. The predicted cleavage site is indicated as *. The polypeptide encoded by the IgkappaLsolCD39 construct has the sequence SEQ ID NO:30. Residues 25-463 are a soluble portion of CD39 and the predicted cleavage of the leader sequence is between Gly20 and Ala21. After expression in recombinant cells, the N-terminal sequence, enzymatic activity, and platelet inhibitory activity is determined for each polypeptide product.

EXAMPLE 12

Development of a Stably Transfected Cell Line Secreting solCD39

A CHO cell line expressing solCD39 was generated to improve recombinant solCD39 polypeptide production.

A. Preparation of Constructs and Cell Lines for the Stable Expression of Soluble CD39 Polypeptides

The solCD39 cDNA insert, containing the recombinant solCD39 sequence and the IL-2 leader but not the FLAG[®] sequence, was excised from the pIL2LSolCD39 plasmid by XmaI/BglII digestion, then inserted into 2A5Ib, an expression vector containing the DHFR gene and optimized for stable CHO cell lines (Morris et al., *In Animal Cell Technology: From Vaccines to Genetic Medicine*, M.J.T. Carrondo, B. Griffiths, and J.L.P. Moreira, editors, Kluwer Academic Publishers, Boston. 529-534, 1997).

The solCD39-2A5Ib plasmid was transfected into CHO cells using Lipofectamine (GIBCO BRL; Gaithersburg, MD) according to manufacturer's recommendations. The CHO cell line used in these studies, DX B-11, had been adapted to serum-free suspension culture conditions. Transfected cells were grown in modified DMEM-F12 medium, supplemented with peptone, glutamine, glucose, transferrin, lipids, and IGF-1 (insulin-like growth factor 1; used solely when cultures were induced for protein expression). After 3 days growth, the cells were transferred to selective medium lacking

hypoxanthine and thymidine. Stock cultures were grown at 37°C in suspension, and passaged every 2-3 days. Induction cultures were grown at 31°C in suspension, with IGF-1 and sodium butyrate (1-2 mM). Cell density at start of induction cultures was $1.5\text{-}2 \times 10^6$ cells/ml. The average induction period was 7 days, at which time CM was collected for further analyses.

5

B. TLC Assays for ADPase and ATPase Activities in CM Containing solCD39

Following growth in selective medium, CM from CHO cell cultures was analyzed for ATPase and ADPase activities. ADPase assays (Marcus et al., *J. Clin. Invest.* 88:1690, 1991) were primarily used in determining enzyme kinetics and pharmacokinetics. Test samples were incubated with 50 μM [^{14}C] ADP (NEN Life Science Products) in assay buffer (15 mM Tris, 134 mM NaCl, 5 mM glucose, pH 7.4, containing 10 μM Ap5A (P^1, P^5 -di[adenosine-5']pentaphosphate, 1 mM ouabain, 10 μM dipyridamole, and 3 mM CaCl_2) in a total volume of 50 μl (5 min, 37°C). Reactions were stopped by placement on ice and addition of 10 μl "stop solution" (160 mM disodium EDTA, pH 7.0, 17 mM ADP, 0.15 M NaCl) to block further metabolism of ADP. Nucleotides, nucleosides, and bases were separated by TLC using isobutanol/1-pentanol/ethylene glycol monoethyl ether/ $\text{NH}_4\text{OH}/\text{H}_2\text{O}$ (90: 60: 180: 90: 120). Radioactivity was quantified by radio TLC scanning (RTLC multiscanner; Packard, Meriden, CT). Results were calculated as averages of duplicate to quadruplicate measurements after subtraction of buffer blanks (consistently <1% of total radioactivity). Data were expressed as percentage of ADP metabolized or as pmol ADP metabolized per minute per μl CM. A unit of activity is the quantity of enzyme which will degrade 1 μmol of ADP in 1 min at 37°C. Identical assays were performed using ATP as a substrate in order to examine the kinetics of the ATPase activity of CD39.

25

As shown in TABLE 6, the stably transfected CHO cells secreted 20-fold higher levels of both enzyme activities compared to CM from transfected COS-1 cells.

TABLE 6
Comparison of ADPase and ATPase Activities in CM Containing solCD39

Cell Type	ADPase (pmol/min/ μl)	ATPase (pmol/min/ μl)
CD39 (CHO)	1403	970
CD39 (COS-1)	70	44

C. Affinity Purification of solCD39 from Stably Transfected CHO Cells

Thirty ml of 10-fold concentrated CM from solCD39-secreting CHO cells was added to 3 ml of B73 mAb-coated Sepharose 4B gel slurry and mixed overnight at 4°C. The affinity matrix was pelleted by centrifugation, washed 3 times with PBS, and added to a plastic column. Specifically-bound protein was eluted by the addition of 0.1 M triethylamine, pH 11.5. Fractions (1.2 ml each) were collected in tubes containing 120 μl of neutralizing solution (1 M sodium phosphate, monobasic; pH 4.3) and analyzed for protein content by SDS-PAGE, followed by Coomassie Blue staining.

35

Biological activity was determined using an ATPase assay as described in Example 7, so that peak fractions could be pooled, buffer exchanged into PBS, and concentrated 5-fold. N-linked sugars were removed from purified protein using a kit from Oxford Glycosystems (Rosedale, NY). The recombinant solCD39 was analyzed by SDS-PAGE.

5 A prominent band of ~66 kD was present in early eluted fractions, with a peak of Coomassie Blue staining around fraction 5 (Fig. 5A). Over 90% of the protein present was found as this major band. Overloading the polyacrylamide gel did reveal some smaller molecular weight contaminants, however, these appear to be related to the antibodies present on the column and not to the protein loaded on the column.

10 ATPDase activity of the affinity column fractions correlated with the intensity of protein bands on SDS-PAGE (Fig. 5A, 5B). ATPDase activity was barely detectable in the anti-CD39 column flowthrough, indicating that affinity purification is an effective means of isolating biologically active recombinant solCD39. Treatment of the purified protein with N-glycanase for 18 hours to remove N-linked oligosaccharides caused the broad band of protein at 66 kD to resolve into a much
15 tighter band of protein at approximately 52 kD, the predicted size for solCD39 (Fig. 5C).

The total protein yield from 1 L of CHO-solCD39 CM was ~2 mg. Production of solCD39 was scaled up to 10 liter bioreactors. The resultant conditioned medium contained approximately 50-100 µg/ml of solCD39 according to ELISA analysis. Thus, each 10 L bioreactor run would expected to produce 500-1000 mg of recombinant polypeptide. CHO cell lines expressing additional solCD39
20 constructs are similarly prepared and characterized.

EXAMPLE 13

Expression of solCD39 in Veggie-CHO and CS-9 Cells

In this example, soluble CD39 is expressed in CHO cells that have been adapted to grow in
25 suspension in media that does not contain animal proteins (see Rasmussen et al., Cytotechnology 28:31, 1998), or in the presence of IGF-1 in the clonal cell line CS-9.

The dihydrofolate reductase-deficient Chinese hamster ovary cell line, DXB11-CHO is commonly used as a host cell for the production of recombinant polypeptides. DXB11-CHO was adapted to grow in suspension. A serum-free host named Veggie-CHO was then generated by
30 adapting DXB11-CHO cells to growth in serum-free media in the absence of exogenous growth factors such as Transferrin and Insulin-like growth factor (IGF-1). The latter adaptation was achieved by a gradual reduction of serum supplementation in the media and the replacement of serum with low levels of growth factors, IGF-1 and transferrin, in an enriched cell growth media. The suspension adapted serum-free adapted cells were then weaned off these growth factors. The resulting Veggie-
35 CHO cells maintain vigorous growth and high viability as well as a DHFR-deficient phenotype in media that is serum-free and also free of animal-derived proteins. CS-9 cells were also derived from DXB11-CHO cells. The suspension adapted serum-free adapted cells were adapted to grow in the

absence of transferrin, then individual clones were isolated. The CS-9 clone was chosen for its stable recombinant protein expression.

Veggie-CHO cells and CS-9 cells are used as a host cell line for the stable, high level expression soluble CD39 polypeptides using methods similar to those described in Example 12.

5

EXAMPLE 14 Biochemical Properties of Affinity-Purified solCD39

Purified solCD39 material was subjected to N-terminal amino acid sequencing and mass spectroscopy. Quantitative amino acid analysis of peak fractions (3-9) from the affinity column yielded a ratio of amino acid residues consistent with calculated values for human CD39. The N-terminus of the pIL2LSolCD39 product had the following sequence:

10

A P T S S S T K K T Q L t s s T Q . . . (residues 25-41 of SEQ ID NO:11).

15

The first 12 residues represent the mature huIL2 residues; residues 13-15 (tss, lower case) are linker-encoded residues; residues 16,17, etc. (T Q . . .) are solCD39.

20

Using the TLC assay system described in Example 12B, the ADPase activity of the membrane-bound HUVEC ecto-ADPase was determined at different pHs in buffers containing 100 mM bis-trispropane (Sigma, St. Louis, MO). This was compared to the ADPase activity of purified solCD39 at these pHs. Kinetic constants for CD39 metabolism of ATP and ADP were determined by measuring the initial rates of reaction as analyzed in the TLC system. ADP or ATP at 2.5-150 μ M were incubated separately with 2×10^{-9} M solCD39.

25

As shown in Fig. 6A, the pH optima for the ecto-ADPase on the surface of HUVEC and for affinity-purified recombinant solCD39 ADPase activities were between pH 8 and 8.5. This indicated that recombinant solCD39 would be maximally active under the same physiological conditions as native CD39/ecto-ADPase .

30

Initial rates of ATP and ADP metabolism by recombinant solCD39 were determined as shown in Fig. 6B, and kinetic constants were derived. The K_m and V_{max} for ADP were 5.9 μ M and 72 pmol/min, respectively; for ATP a K_m of 2.1 μ M and V_{max} of 26 pmol/min were determined. The assays were performed with 2×10^{-9} M solCD39, yielding k_{cat} of 720 min^{-1} (ADP) and 260 min^{-1} (ATP). Thus, the specificity constant, k_{cat}/K_m ($1.2 \times 10^8 \text{ min}^{-1} \text{ M}^{-1}$), was identical for ADP and ATP. The specific activity for purified recombinant solCD39 was 11 U/mg for ADP and 4 U/mg for ATP.

35

EXAMPLE 15 Platelet Inhibitory Properties of solCD39

This example shows that recombinant affinity purified solCD39 is effective as an inhibitor of platelet activation and recruitment.

After obtaining informed consent from volunteers, blood was collected via plastic tubing using acid citrate-dextrose (38 mM citric acid; 75 mM sodium citrate; 135 mM glucose) as

anticoagulant. Where indicated, volunteers had ingested 650 mg acetylsalicylic acid (ASA) 18 h prior to blood donation. Platelet-rich plasma (PRP) was prepared with an initial whole blood centrifugation (200g, 15 min, 25°C), and a second centrifugation of the PRP (90 g, 10 min) to eliminate residual erythrocytes and leukocytes. The stock suspension of PRP was maintained at room temperature under 5% CO₂-air.

A. Platelet Aggregation Studies

PRP containing 1.22×10^8 platelets was pre-incubated (3 min, 37°C) in an aggregometer cuvette (Lumiaggregometer; Chrono-Log, Havertown, PA) alone or in combination with test samples containing solCD39. Total volumes were adjusted to 300 µl with TSG buffer (Marcus et al., *J. Clin. Invest.* 88:1690, 1991; Marcus et al., *J. Clin. Invest.* 99:1351, 1997). After the 3 min preincubation, platelet agonists (ADP or collagen) were added at the concentrations indicated, and the aggregation response recorded for 4-5 min. Where indicated, 10 µM indomethacin (Sigma, St. Louis, MO) was added to PRP to inhibit endogenous cyclooxygenase activity.

As shown in Fig. 7, the addition of 10 µM ADP to PRP alone resulted in a full, irreversible aggregation response; partially reversible aggregation occurred at lower ADP concentrations. However, in the presence of only 3.3 µg/ml solCD39, platelet aggregation induced by 10 µM ADP was abruptly terminated and the curve rapidly returned to baseline. Importantly, the extent of aggregation was reduced to levels below those observed with 1 µM ADP. Higher concentrations of solCD39 had an even more profound inhibitory effect, virtually eliminating the initial burst of aggregation elicited by 10 µM ADP.

Platelet responsiveness to 5 µM ADP was examined in PRP treated with and without the cyclooxygenase inhibitor indomethacin (10 µM), in the presence of CM containing solCD39 from COS-1 and CHO cells. As shown in Fig. 8A, indomethacin treatment resulted in partial reversal of ADP-induced platelet aggregation in the absence of solCD39. In contrast, CM containing solCD39 were capable of completely abrogating platelet responses to ADP, whether PRP was indomethacin-treated or not.

Inhibition of platelet reactivity by CD39 was not limited to blocking the agonistic effects of ADP, as shown in Fig. 8B and 8C. Collagen, which is another critical platelet agonist, was used at 1 µg/ml to induce platelet aggregation. The presence of solCD39 markedly reduced the response to collagen compared to control (Fig. 8B, upper curves). A similar inhibitory effect of solCD39 was observed in PRP treated with indomethacin (Fig. 8B, lower curves), when collagen was used at 3.3 µg/ml. As shown in Fig. 8C, the effect of solCD39 on collagen-induced aggregation was dose dependent.

B. Inactivation of Enzymatic Activity of solCD39 and the Effect on Inhibition of Platelet Activation

To demonstrate that the ability of solCD39 to inhibit platelet activation and recruitment was due to the enzymatic activity of solCD39 and not to some other property, the solCD39 was reacted

with FSBA (Fluorosulfonylbenzoyl-adenosine), an ATP analog that inhibits collagen-induced platelet activation (Colman et al., *Blood* 68:565, 1986) and binds irreversibly with ATPDases found on several cell types (Sevigny et al., *Biochem. Biophys. Acta* 1334:73, 1997; Sevigny et al., *Biochem. J.*, 312:351, 1995).

5 SolCD39 (2 nmol) was combined with 2 ml labeling buffer (100 mM Hepes, pH 7.4, 200 mM NaCl, 4% dimethylformamide [vol/vol]), 400 μ l 5 mM FSBA (Sigma Chemical Co.) dissolved in ethanol, and 1.52 ml water. A mock-treated sample was also prepared in which the FSBA solution was replaced with water. After incubating at 37° for 90 min., the samples were centrifuged in a Centricon-10 filter unit (Amicon Corp.) for 1 hour at 5,500 rpm and buffer exchanged into PBS to
10 remove unreacted material. The effect of FSBA-treated solCD39 on platelet reactivity is shown in Figure 9.

Induction of platelet activation by ADP (Fig. 9A) or collagen (Fig. 9B) was significantly inhibited by either purified solCD39 or mock FSBA-treated solCD39. In contrast, incubation with FSBA-treated solCD39 did not have a significant effect on platelet activation. A comparative titration
15 of mock-treated solCD39 verses FSBA-treated solCD39 (Fig. 9C) indicated that 22.0 μ g/ml of FSBA-treated sol CD39 gave a similar aggregation profile as 0.88 μ g/ml of mock-treated solCD39. This indicated that 96% of the aggregation inhibitory activity of solCD39 was lost after FSBA derivitization. Analyses of residual ADPase activity of FSBA- treated solCD39 by the radio-TLC assay system demonstrated that approx. 94% of the enzymatic activity was blocked, while the
20 phosphate release assay indicated that a similar percentage of the ATPase activity was lost as well.

C. Mutagenesis Studies

To identify amino acids involved in the biological activity of solCD39, site directed mutagenesis was used to alter selected amino acid residues in CD39. Mutants were assayed for
25 enzymatic (ATPase and ADPase) and platelet inhibitory (dose-dependent inhibition of platelet aggregation) activities. For one series of mutants, residues within the conserved apyrase regions were replaced with alanine.

Platelet inhibitory activity correlated generally with enzymatic activity. The E174A mutant (residues are numbered as in Figure 1) was completely devoid of enzymatic activity and had no effect
30 on platelet responsiveness; the S218A mutant retained less than 10% of ADPase activity and approx. 10% of platelet inhibitory activity. Glutamate174 and Serine218 therefore appear to be important for both the enzymatic and platelet inhibitory activities of CD39.

Additional mutant forms of CD39 are expressed and assayed for enzymatic and platelet inhibitory activity in order to identify mutants with increased or decreased activity as well as mutants
35 that preferentially catalyze the ATPase or ADPase reaction.

EXAMPLE 16**Persistence of solCD39 Following In Vivo Administration in Mice**

Balb/c mice (6-8 weeks of age; maintained under specific pathogen-free conditions; Jackson Laboratory, Bar Harbor, ME) were intravenously injected with 50 µg recombinant solCD39 in 100 µl sterile saline (0.9% NaCl). No overt external difficulties were noted in the animals following injection. At various times after injection (5, 10, 30 min, 1, 2, 4, 8, 24 h), pairs of mice were bled by cardiac puncture and euthanized. Serum was prepared from each blood sample and frozen until assay. The presence of biologically active solCD39 in serum samples was measured in ATPase and ADPase assays. The data were fit using Deltagraph (Deltapoint, Monterey, CA). The best fit was derived using double exponential decay. Where indicated, specificity of enzyme activity was determined by incubating serum samples with anti-CD39 mAb-coated beads to remove CD39 prior to testing for ATPase activity.

As shown in Fig. 10, the data obtained best fit a biphasic exponential curve. The amount of ATPase activity from 25 µg/ml of solCD39 placed in murine serum is presented for comparison. The $t_{1/2\alpha}$ (distribution phase) was calculated to be 59 min in the ATPase assay and 43 min in the ADPase assay. Approximately 55-65% of apyrase activity was cleared from the circulation during this phase. The elimination phase had a $t_{1/2\beta}$ of approximately 40 h in both assays. Preclearing the 10 min, 2h, and 24 h time point samples with anti-CD39 mAb-coated beads completely eliminated serum ATPase/ADPase activities. These data also demonstrate that the assays specifically detect recombinant human solCD39.

EXAMPLE 17**Pilot Dose Ranging Study in Yorkshire-Hampshire Pigs**

SolCD39 was administered to Yorkshire-Hampshire pigs, which have been developed as a porcine model of thrombosis. Following intravenous injection, CD39 persisted in the circulation and was capable of inhibiting platelet aggregation and recruitment for as much as a week following injection. This is in marked contrast to many other therapeutic agents used for platelet inhibition, wherein the duration of inhibition is very short.

Ten pigs were randomly assigned to receive solCD39 in low (72 µg/kg), medium (221 µg/kg), or high (670 µg/kg) doses. Aspirin was administered orally on a daily basis. Placebo controls consisted of aspirin. Saline controls and solCD39 were administered as a single bolus. Time points were measured following this administration. Blood samples were obtained via an external jugular vein catheter. Bleeding times were measured in pigs receiving placebo controls and in those receiving solCD39 at baseline and at 60 minutes. ADP-induced platelet aggregation was measured at specific time intervals following administration. The concentration of CD39 in serum as a function of time was measured using an ELISA assay.

Administration of solCD39 was well tolerated. It did not induce anemia or thrombocytopenia and, importantly, a second dose of solCD39 could be administered without observable ill effects, such

as hypotension, thrombocytopenia, or hemorrhage. Clot retraction was normal following all experiments, indicating that platelet function was essentially normal.

A. Effect of solCD39 on Bleeding Time

5 Bleeding time is an absolute measure of platelet function. As shown in Figure 11, solCD39 induced a prolonged bleeding time. This indicated that a therapeutic effect had been obtained via a mild interference with platelet function. These mild increases in bleeding time were similar to those obtained by aspirin administration. This indicates that the hemorrhagic defect was mild.

10 B. Effects of Aspirin and solCD39 on Platelet Aggregation

Figure 12A shows the effect of aspirin on platelet aggregation at baseline and at day 5, and Figure 12B shows the effect of high dose solCD39 on platelet aggregation at baseline and at day 7. Peak heights from the platelet aggregation curves for each of the three solCD39 doses are plotted in Fig. 13. The platelet aggregation data are also compared by plotting relative areas from the platelet aggregation curves for each of the three solCD39 doses. A dose of 670 $\mu\text{g/kg}$ inhibited greater than 90% of ADP induced platelet aggregation. The inhibitory effect was long-lived, with 30% inhibition (after high dose solCD39) at two weeks. These experiments show that solCD39 has potent and long lasting anti-platelet effects, and that these effects are superior to those obtained using aspirin.

20 C. Persistence of solCD39 in Serum

The persistence of solCD39 in porcine serum, as determined by ELISA, is shown in Fig. 14. Distribution and clearance half-lives were determined using a biphasic curve fit. The $t_{1/2\alpha}$ (distribution phase) was calculated to be 29 minutes. The elimination phase had a $t_{1/2\beta}$ of approximately 51 hours. SolCD39 biological activity (ADPase activity) also exhibited a long elimination half-life, approaching 5-7 days, and could still be detected over two weeks after administration. During this time there were no changes in hematologic parameters and no evidence of hemorrhage despite tripling of the bleeding time.

D. Percutaneous Transluminal Coronary Angioplasty (PTCA) Study

30 Porcine platelets and fibrinogen were labeled with $^{111}\text{Indium}$ and $^{125}\text{Iodine}$ respectively for infusion into pigs. Twelve pigs were sedated and anesthetized, and randomly assigned to receive intravenous solCD39 (670 $\mu\text{g/kg}$) plus heparin and ASA or intravenous saline placebo plus heparin and ASA. Oral ASA was given to all pigs for at least three day prior to the coronary angioplasty procedure, and heparin (100 U/kg) was given at the time of the angioplasty. One to three days prior to the angioplasty an external jugular line was inserted to administer the labeled platelets and fibrin, CD39 or saline, and to facilitate blood draws. Labeled platelets and fibrinogen were given approximately 18 hours prior to balloon injury. Coronary arteries were injured using an oversize

balloon. A coronary guide catheter was first advanced into the ascending aorta. An oversized balloon was then advanced into a coronary vessel and inflated at 6 to 8 atmospheres for a total of thirty seconds. The balloon was then deflated and withdrawn. The average ratio of balloon size to vessel size was 1.32 for the placebo group and 1.29 for the CD39 group.

Platelet aggregation and bleeding time were measured 30 minutes after administration. The pigs were killed 24 hours after balloon injury and solCD39 administration, and the labeled platelet ($^{111}\text{Indium}$) and fibrin ($^{125}\text{Iodine}$) deposition per cm^2 was measured in the injured coronary artery segments. The results are summarized in TABLE 7. CD39 administration was well tolerated without bleeding or hemodynamic complications. Moreover, no bleeding was noted during PTCA or after sheath removal and there was no significant difference in hematocrit or platelet counts between the groups.

These results show that the administration of solCD39 results in a significant inhibition of platelet aggregation and prolongation of bleeding time, as well as a trend toward inhibition of platelet and fibrin deposition, after balloon injury in animals. The results also suggest that CD 39 has a minimal risk of inducing bleeding.

TABLE 7
Effects of solCD39 After Balloon Injury

Treatment	Platelet Deposition Ratio	Fibrin Deposition Ratio	Bleeding Time	% Inhibition of Platelet Aggregation
Placebo	1.78 ± 0.4	0.71 ± 0.14	3.03 ± 0.2	1 ± 10
solCD39	1.25 ± 0.19	0.62 ± 0.10	7.00 ± 0.81	80 ± 2
p=	0.2	0.5	0.009	0.001

After the radioactivity decayed, toluidine-blue stained injured coronary artery segments were examined histologically, in order to further characterize the extent of thrombus formation. A blinded observer qualitatively evaluated the degree of histologic injury in the coronary segments by assessing, on a scale of 1-4 with 4 being the most severe injury, the severity of medial and internal elastic lamina tear, medial separation, and hemorrhage. A composite injury score was obtained by totaling the three individual scores. The medial injury scores for the placebo and CD39 groups were 2.5 and 2.2 respectively; medial separation scores for the placebo and CD39 groups were 2.0 and 1.6 respectively; the degree of hemorrhage for the placebo and CD39 groups were 2.3 and 2.5 respectively. The composite injury scores for the placebo and CD39 groups were 6.6 and 6.2 respectively. These in vivo results correlate well with results, reported herein, obtained in vitro and ex vivo.

EXAMPLE 18 Soluble CD39 Provides Additive Inhibition of Platelet Aggregation Over Aspirin and Abciximab

An ex vivo study was performed in order to evaluate the additive inhibition of platelet aggregation when soluble CD39 is added to platelet rich plasma from patients receiving: placebo,

aspirin, clopidogrel, ticlopidine, or abciximab. Each group consisted of three to six patients. The clopidogrel, ticlopidine, and abciximab groups also received aspirin. Baseline platelet aggregation was measured for each group, in response to the platelet agonists ADP, collagen, or the Thrombin Receptor Activating Peptide TRAP₁₋₆. SolCD39 (10 µg/ml or 100 µg/ml) was then added and the additional inhibition of platelet activation (over baseline, in response to the platelet agonists) was measured in each of the five groups. The result are shown in TABLE 8.

TABLE 8
Additive Inhibition of Platelet Aggregation by Soluble CD39

	Group				
	Placebo	Aspirin	Clopidogrel	Ticlopidine	Abciximab
Baseline					
ADP	84 ± 4 ¹	69 ± 5	58 ± 6	76 ± 3	0 ± 0
Collagen	85 ± 1	62 ± 8	57 ± 9	71 ± 17	0 ± 0
TRAP	94 ± 2	66 ± 6	51 ± 2	26 ± 5	46 ± 6
SolCD39 10 µg/ml					
ADP	0 ± 0 100% ²	4 ± 2 97%	5 ± 2 92%	10 ± 2 86%	0 ± 0 100%
Collagen	75 ± 2 11%	21 ± 4 68%	31 ± 9 48%	48 ± 18 37%	0 ± 0 100%
TRAP	70 ± 3 26%	38 ± 7 45%	35 ± 1 31%	19 ± 6 33%	22 ± 10 52%
SolCD39 100 µg/ml					
ADP	0 ± 0 100%	1 ± 0 99%	0 ± 0 100%	2 ± 2 97%	0 ± 0 100%
Collagen	57 ± 5 33%	16 ± 4 75%	21 ± 6 64%	37 ± 15 53%	0 ± 0 100%
TRAP	65 ± 4 30%	26 ± 5 63%	23 ± 3 55%	18 ± 7 36%	22 ± 9 52%

¹Platelet aggregation, arbitrary units

²Percent inhibition relative to same agonist in the absence of CD39

Soluble CD39 at a concentration of 10 µg/ml synergistically inhibited ADP, collagen, and TRAP mediated platelet aggregation in patients on aspirin ($p < 0.001$), and this effect was independent of clopidogrel and ticlopidine. Abciximab alone abolished platelet aggregation due to ADP and collagen, but CD39 provided synergistic inhibition of platelet aggregation induced by TRAP ($p < 0.007$). Soluble CD39 at 100 µg/ml provided increased inhibition of platelet aggregation to all agonists. These results were also seen in vitro. Collagen and TRAP induce platelet aggregation via mechanisms in addition to ADP release and recruitment, so the ability of CD39 to inhibit collagen and TRAP-mediated platelet aggregation suggests additional versatility of CD39 as an antithrombotic agent.

EXAMPLE 19
Soluble CD39 Inhibits Thrombosis and Limits Ischemic Cerebral Injury
in Wild Type and Reconstituted CD39 Null Mice

The above examples suggested that soluble CD39 would inhibit ADP-mediated amplification of platelet recruitment in distal microvessels, thereby reducing thrombosis after stroke. The following experiments illustrate the use of CD39 in a microvascular thrombosis (murine ischemic stroke) model. Soluble CD39 inhibited microvascular thrombosis and conferred cerebroprotection in stroke. A notable feature of the solCD39 treatment was the low incidence of intracerebral hemorrhage relative to that reported for other antithrombotic agents.

A. Materials and Methods

C57BL/6J mice (6-8 wk) were obtained from Jackson Laboratories (Bar Harbor, ME). Untreated mice, and mice treated with 4 mg/kg solCD39, with 5 mg/kg aspirin or phosphate buffered saline, were anesthetized and heparinized (10 U/g), prior to blood collection via cardiac puncture. 80 μ L of 3.8% trisodium citrate was added to each mL of blood. Samples from 6-8 mice were pooled and platelet-rich plasma (PRP) was prepared by centrifugation. The PRP contained 400-700 $\times 10^3$ platelets per μ L. All experiments were completed within 2 hours of blood collection. PRP (200 μ L) was preincubated, for 3 min. at 37°C, with 100 μ L Tris-buffered saline buffer (15 mM NaCl, 5 mM glucose, pH 7.4) in an aggregometer cuvette (Lumiaggregometer; Chrono-Log, Havertown, PA), and the platelet agonists ADP, collagen, or sodium arachidonate were added at the final concentrations indicated. Aggregation responses were recorded for 2-4 min, and expressed as area under the curve (height times width at 1/2 height).

The effects of soluble CD39 were tested in a previously validated murine model of stroke injury (Choudhri, T.F., et al., *J. Clin. Invest.* 102:1301-1310 (1998); Connolly, E.S., Jr., et al., *J. Clin. Invest.* 97:209-216 (1996); and Connolly, E.S., Jr., et al., *Neurosurg.* 38(3):523-532 (1996)). Anesthetized mice were maintained at 37 \pm 2°C during and for 90 min following surgery. A midline neck incision was made and the right carotid artery exposed. Middle cerebral artery occlusion was accomplished by advancing a 13-mm heat-blunt tipped 6-0 nylon suture via an arteriotomy in the external carotid stump. The external carotid artery was cauterized to secure hemostasis, and arterial flow re-established. Carotid artery occlusion never exceed 3 min. The occluding suture was removed after 45 min and cautery was again locally applied to prevent bleeding at the arteriotomy site. Surgical staples were used for wound closure.

Doppler measurement of cerebral cortical blood flow, neurological score (Huang, Z., et al., *Science* 265:183-1885 (1994)), calculation of infarct volume, measurement of cerebral thrombosis using ¹¹¹In-labeled platelets (Choudhri, T.F., et al., *J. Clin. Invest.* 102:1301-1310 (1998) and Naka, Y., et al., *Circ. Res.* 76:900-906 (1995)), detection of intracerebral fibrin (Choudhri, T.F., et al., *J. Clin. Invest.* 102:1301-1310 (1998)), and measurement of intracerebral hemorrhage (Choudhri, T.F., et

al., *J. Clin. Invest.* 102:1301-1310 (1998) and Choudhri, T.F., et al., *Stroke* 28:2296-2302 (1997)) were measured as previously described. The results are described below.

B. Soluble CD39 Abrogates the Ex Vivo Aggregation of Murine Platelets

Platelet-rich plasma was obtained from mice 1 hour after injection of saline (vehicle), soluble CD39, or aspirin. Ex vivo platelet aggregation was studied to ascertain the relative potency of solCD39 as compared to aspirin (which can improve the outcome following a transient ischemic attack). Platelets from control and aspirin-treated mice strongly aggregated following stimulation with ADP (Fig. 15A) or collagen (Fig. 15B).

Soluble CD39 abrogated platelet aggregation in the presence of ADP, and attenuated aggregation in the presence of collagen and arachidonate. In contrast, aspirin treatment only blocked platelet reactivity to arachidonate (Fig. 15C). The platelets from mice pretreated with solCD39 showed an initial aggregation in the presence of arachidonate, but rapidly disaggregated and returned to the resting state before a full response occurred (Fig. 15C).

C. Soluble CD39 Is Effective Even When Added at the Peak of the Aggregation Response

ADP (5 μ M) was added to mouse platelets in vitro to induce an aggregation response. Soluble CD39 (2.5 μ g/ml or 1.25 μ g/ml) was added at the peak of the aggregation response. The solCD39 immediately reversed the aggregation response, as shown in Fig. 16. This result demonstrates that SolCD39 is able to reverse an aggregation response, rapidly returning platelets to a resting state, even when added at the peak of the response. This result likely reflects the fact that at the peak of the aggregation response ADP is prominent in the releasate from the aggregating platelets. Soluble CD39 metabolizes this ADP to the biologically inactive compound AMP almost instantaneously, accounting for the rapid descent of the aggregation curve in Fig. 16, right side.

D. Soluble CD39 Reduces the Sequelae of Stroke

Intravenously injected soluble CD39 showed therapeutic utility in stroke. Soluble CD39 inhibited platelet accumulation in the ipsilateral cerebral hemisphere following induction of stroke, as shown in Fig. 17A. Similarly, solCD39 decreased the level of fibrin accumulation in the ipsilateral hemisphere (vs. contralateral) as measured by Western blot analysis using a fibrin specific antibody (Fig. 17B).

The ability of solCD39 to reduce thrombosis, as measured by decreased platelet and fibrin deposition, was accompanied by improved postischemic cerebral perfusion 24 hours after stroke induction, as shown in Fig. 18A. In contrast, when aspirin was administered at a clinically relevant dose (that inhibited the *ex vivo* response of platelets to arachidonate) no improvement was seen in postischemic cerebral blood flow (Fig. 18A).

Preoperatively administered solCD39 conferred a dose-dependent diminution of cerebral infarct volume, as measured by digital histological analysis (Fig. 18B). Aspirin, in contrast, showed a

tendency to decrease cerebral infarct volume, although this effect was not statistically significant. The administration of soluble CD39 either prior to, or up to 3 h following, stroke reduced both neurological deficit (Fig. 18C) and mortality (Fig. 18D).

The effects of soluble CD39 and aspirin on the development of intracerebral hemorrhage following stroke are shown in Fig. 18E. Aspirin increased intracerebral hemorrhage (as measured spectrophotometrically) significantly, but there was no significant increase in intracerebral hemorrhage at any dose of soluble CD39 tested. At these doses, soluble CD39 inhibited both platelet and fibrin accumulation and promoted an increase in postischemic blood flow, as shown in Figs. 17A, 17B, and 18A. Figure 19 shows a covariate plot of cerebral infarct volume vs. intracerebral hemorrhage for each treatment, and indicates that aspirin is less capable of reducing infarct volume and preventing intracerebral hemorrhage than soluble CD39. In summary, at the doses tested in the mouse stroke model, solCD39 conferred protection without inducing the bleeding problems that often accompany anti-thrombotic therapy regimens.

E. CD39 Null Mice Can be Reconstituted with Soluble CD39

CD39^{-/-} mice were generated using a gene targeting vector in which exons 4-6, encoding apyrase conserved regions 2-4 (Handa, M. & Guidotti, G., *Biochem. Biophys. Res. Commun.* 218:916-923 (1996); Wang, T.F. & Guidotti, G., *J. Biol. Chem.* 271:9898-9901 (1996); Maliszewski, C.R., et al., *J. Immunol.* 153:3574-3583 (1994); and Schoenborn, M.A., et al., *Cytogen Cell Gen.* 81(3-4):287-280 (1998)), were replaced with a PGKneo cassette, as shown in Fig. 20A. The gene targeting vector, in which a 4.1 kb *SpeI-BglIII* fragment containing exons 4-6 was replaced with a PGKneo cassette, was introduced into 129-derived ES cells. Cells were selected in G418 and gancyclovir. Nine ES clones with a disrupted CD39 allele, as identified by genomic Southern blot analyses of *BglIII* digested DNA as shown in Fig. 20B, were injected into blastocysts and the resulting chimeras crossed to C57BL/6 to produce CD39^{+/-} heterozygotes. CD39^{-/-} mice were generated at the expected Mendelian frequency from CD39^{+/-} intercrosses. The CD39^{-/-} mice used in the experiments described below represent random C57BL/6 x 129 hybrids.

Homozygous CD39^{-/-} mice were overtly normal, and did not display an obvious phenotype in the unperturbed state. Hematological profiles, including erythrocyte parameters, platelet counts, leukocyte counts and differentials, and coagulation screening, were normal. As shown below, the CD39-null mice did not exhibit a prothrombotic phenotype unless challenged by experimental stroke. Under those conditions, the defect was abolished and normal blood fluidity was restored by administration of soluble CD39. Bleeding times of CD39^{-/-} mice were normal, indicating that normal blood flow in an unperturbed animal is not dependent upon endogenous expression of CD39. As is seen in normal mice, CD39^{-/-} animals exhibited markedly increased bleeding times following the administration of aspirin or following administration of increasing doses of solCD39 as shown in Fig. 21. CD39^{-/-} mice subjected to focal cerebral ischemia exhibited diminished blood flow following reperfusion as compared to genetically matched controls (Fig. 22A), indicating that endogenous CD39

contributes to maintenance of hemostasis during episodes of vascular injury. When solCD39 (8 mg/kg) was administered to the CD39^{-/-} mice, these mice were “reconstituted” as shown by a postischemic blood flow similar to untreated controls. CD39^{-/-} mice demonstrated increased cerebral infarction volume as compared to genotype-matched controls following induced stroke (Fig. 22B).

5 CD39^{-/-} mice “reconstituted” with solCD39 had markedly diminished infarct volume, indicating a protective effect of solCD39. Other parameters (neurological deficit scores, overall mortality, and intracerebral hemorrhage) did not differ between groups (Fig. 22 C, D, E).

These results demonstrate that CD39 inhibits microvascular thrombosis and confers cerebroprotection without inducing intracerebral hemorrhage in a murine model of stroke. Soluble
10 CD39 decreased platelet deposition, fibrin deposition, and cerebral infarction volume. Soluble CD39 reduced infarction volume and restored postischemic blood flow even when administered three hours following stroke induction. This result is important because the average patient experiencing a stroke appears in the emergency room approximately three hours after the initial event occurs. The ability to treat patients with solCD39 after three hours provides an important advantage over many other agents
15 designed to inhibit platelet reactivity.

EXAMPLE 20

Soluble CD39 Improves Survival in a Mouse Ischemia Model

C57BL/6 mice were anesthetized and ventilated, and their thoraces were opened to surgically
20 expose both pulmonary hila. Either physiological saline or soluble CD39 (8 mg/kg) was administered intravenously, after which the left pulmonary hilum was cross-clamped for one hour. The cross-clamp was removed for three hours of reperfusion, and then a cross-clamp was applied to the right hilum for a thirty minute observation period. This latter maneuver effectively removed the normal lung from circulation, so that the mouse must survive on the function of the post-ischemic left lung. The results
25 are shown, in the form of a Kaplan-Meier survival plot, in Figure 23. All of the mice given saline (n=6) died prior to the thirty minute time point whereas all of the sol39-treated mice (n=3) survived for thirty minutes.

The long lasting effects of soluble CD39 are also shown to be clinically useful in the reduction of complications of atherosclerosis, such as myocardial infarction, stroke, and peripheral
30 vascular occlusion. Patients suffering from these conditions demonstrate an abundance of activated platelets in their circulation, and such activated platelets have a lowered threshold for ADP stimulation. Soluble CD39 metabolically deletes ADP from the fluid phase of activated platelets and reverses their prothrombotic characteristics.

The relevant disclosures of publications cited herein are specifically incorporated by
35 reference. The examples presented above are not intended to be exhaustive or to limit the scope of the invention. The skilled artisan will understand that variations and modifications and variations are possible in light of the above teachings, and such modifications and variations are intended to be within the scope of the invention.

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CLAIMS**We claim:**

1. A method for inhibiting platelet activation and recruitment in a mammal in need of such treatment comprising administering an effective amount of a soluble CD39 polypeptide having a structure X-Y wherein X is selected from the group consisting of an Ala residue and heterologous peptides capable of adopting a stable secondary structure and Y is selected from the group consisting of:

(a) polypeptides having an amino acid sequence as set forth in (SEQ ID NO:2) wherein the amino terminus is selected from the group consisting of amino acids 36-44, and the carboxy terminus is selected from the group consisting of amino acids 471-478;

(b) fragments of the polypeptides of (a) wherein said fragments have apyrase activity; and

(c) variants of the polypeptides of (a) or (b), wherein said variants have apyrase activity.

2. The method of claim 1 wherein Y is selected from the group consisting of:

(a) polypeptides having a sequence consisting of amino acids 38-476 or 39-476 of SEQ ID NO:2,

(b) variant polypeptides that are at least 70% identical in amino acid sequence to amino acids 36 to 478 of SEQ ID NO:2 or to a fragment thereof, wherein said variant polypeptides have apyrase activity;

(c) variant polypeptides that are at least 80% identical in amino acid sequence to amino acids 36 to 478 of SEQ ID NO:2 or to a fragment thereof, wherein said variant polypeptides have apyrase activity;

(d) variant polypeptides that are at least 90% identical in amino acid sequence to amino acids 36 to 478 of SEQ ID NO:2 or to a fragment thereof, wherein said variant polypeptides have apyrase activity;

(e) variant polypeptides that are at least 95% identical in amino acid sequence to amino acids 36 to 478 of SEQ ID NO:2 or to a fragment thereof, wherein said variant polypeptides have apyrase activity;

(f) variant polypeptides that are at least 98% identical in amino acid sequence to amino acids 36 to 478 of SEQ ID NO:2 or to a fragment thereof, wherein said variant polypeptides have apyrase activity; and

(g) variant polypeptides that are at least 99% identical in amino acid sequence to amino acids 36 to 478 of SEQ ID NO:2 or to a fragment thereof, wherein said variant polypeptides have apyrase activity.

3. The method of claim 1 wherein X is a peptide fragment from the amino terminal portion of mature IL-2, CD39-L2, CD39-L3, or CD39-L4.

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4. The method of claim 1 comprising administering a polypeptide having the structure A-B-Y wherein A is 0-20 amino acids from the amino terminal portion of mature IL-2 and B is a linker of 0-15 amino acids.

5. A method of inhibiting platelet activation and recruitment in a mammal in need of such treatment comprising administering an effective amount of a soluble CD39 polypeptide selected from the group consisting of:

(a) SEQ ID NO: 6, amino acids 25-464 of SEQ ID NO:27, amino acids 25-474 of SEQ ID NO:28, amino acids 27-473 of SEQ ID NO:29, amino acids 21-476 of SEQ ID NO:3, amino acids 21-476 of SEQ ID NO:4, or amino acids 21-463 of SEQ ID NO:30; and

(b) fusion polypeptides comprising the polypeptides of (a), wherein said fusion polypeptides have apyrase activity.

6. The method of claim 5 wherein the soluble CD39 polypeptide has an amino acid sequence selected from the group consisting of SEQ ID NO: 6, amino acids 25-464 of SEQ ID NO:27, amino acids 25-474 of SEQ ID NO:28, amino acids 27-473 of SEQ ID NO:29, amino acids 21-476 of SEQ ID NO:3, amino acids 21-476 of SEQ ID NO:4, and amino acids 21-463 of SEQ ID NO:30.

7. The method of claim 6 wherein the soluble CD39 polypeptide has the sequence of amino acids 21-463 of SEQ ID NO: 30.

8. A method according to one of claims 1-7 wherein the soluble CD39 polypeptide has been produced by culturing a recombinant cell that encodes the soluble CD39 polypeptide under conditions permitting expression of the CD39 polypeptide, and recovering the expressed CD39 polypeptide:

9. The method of claim 8 wherein the recombinant cell comprises a nucleic acid having a sequence selected from the group consisting of:

(a) SEQ ID NO:5; and

(b) DNA sequences which, due to degeneracy of the genetic code, encode the polypeptide encoded by SEQ ID NO:5.

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10. The method of claim 8 wherein the recombinant cell comprises a nucleic acid having a sequence selected from the group consisting of:

(a) SEQ ID NO:7; and

(b) DNA sequences which, due to degeneracy of the genetic code, encode the polypeptide encoded by SEQ ID NO.7.

11. The method of one of claims 1-10 wherein the soluble CD39 polypeptide is administered in a composition comprising a pharmaceutically acceptable carrier.

12. The method of one of claims 1-11 wherein the soluble CD39 polypeptide is administered in combination with at least one other antithrombotic or antiplatelet composition.

13. The method of claim 12 wherein the soluble CD39 polypeptide is administered in combination with aspirin.

14. The method of one of claims 1-13 wherein the soluble CD39 polypeptide is administered parenterally.

15. The method of claim 14 wherein the soluble CD39 polypeptide is administered intravenously.

16. The method of one of claims 1-15 wherein the mammal is suffering from unstable angina, myocardial infarction, stroke, coronary artery disease or injury, myocardial infarction, atherosclerosis, peripheral vascular occlusion, preeclampsia, embolism, a platelet-associated ischemic disorder including lung ischemia, coronary ischemia, and cerebral ischemia, a thrombotic disorder including coronary artery thrombosis, cerebral artery thrombosis, intracardiac thrombosis, peripheral artery thrombosis, venous thrombosis, thrombosis and coagulopathy associated with exposure to a foreign or injured tissue surface, deep venous thrombosis (DVT), pulmonary embolism (PE), transient ischemic attack (TIAs), or another related condition where vascular occlusion is the common underlying feature.

17. The method of one of claims 1-15 wherein the soluble CD39 is administered to prevent thrombus formation or reformation, occlusion, reocclusion, stenosis, or restenosis of blood vessels, or stroke.

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18. The method of one of claims 1-15 wherein the soluble CD39 is administered in conjunction with angioplasty, carotid endarterectomy, anastomosis of vascular graft, atherectomy, stent placement, placement of a chronic cardiovascular device such as an in-dwelling catheter or prosthetic valve or vessel, or bypass surgery.

19. A method for degrading nucleoside tri- and/or di- phosphates in a mammal in need of such treatment comprising administering an effective amount of a soluble CD39 polypeptide having a structure X-Y wherein X is selected from the group consisting of an Ala residue and heterologous peptides capable of adopting a stable secondary structure and Y is selected from the group consisting of:

(a) polypeptides having an amino acid sequence as set forth in (SEQ ID NO:2) wherein the amino terminus is selected from the group consisting of amino acids 36-44, and the carboxy terminus is selected from the group consisting of amino acids 471-478;

(b) fragments of the polypeptides of (a) wherein said fragments have apyrase activity; and

(c) variants of the polypeptides of (a) or (b), wherein said variants have apyrase activity.

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Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn Ile Leu Ala 19
Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu Leu Ala Val Gly Leu Thr 38
 Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser 57
 Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly 76
 Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val 95
 Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu 114
 Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly 133
 Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val 152
 Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly 171
 Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser 190
 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe 209
 Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln 228
Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn 247
 Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu 266
 Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro 285
 Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg 304
 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln 323
 Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln 342
 Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser 361
 Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu 380
 Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr 399
 Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr 418
 Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile 437
 His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu 456
Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser 475
Thr Tyr Val Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile 494
Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val 510

Fig. 1

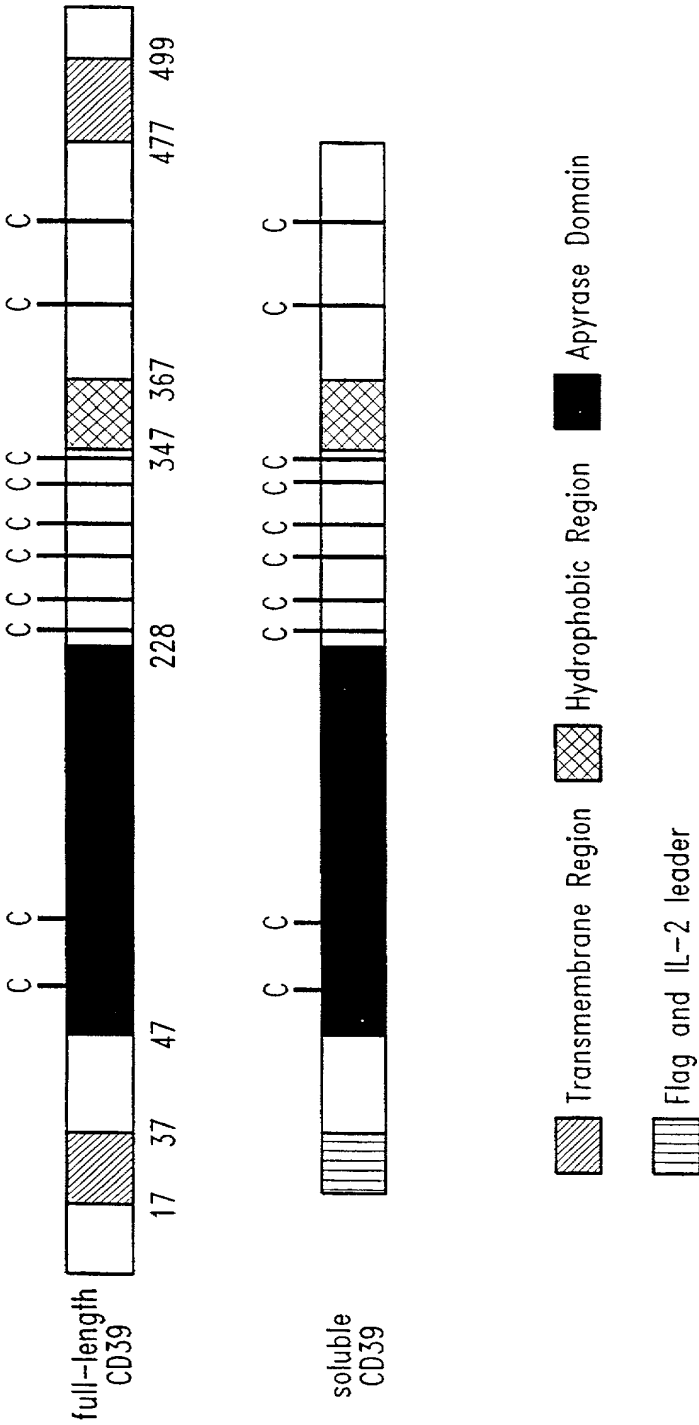


Fig. 2

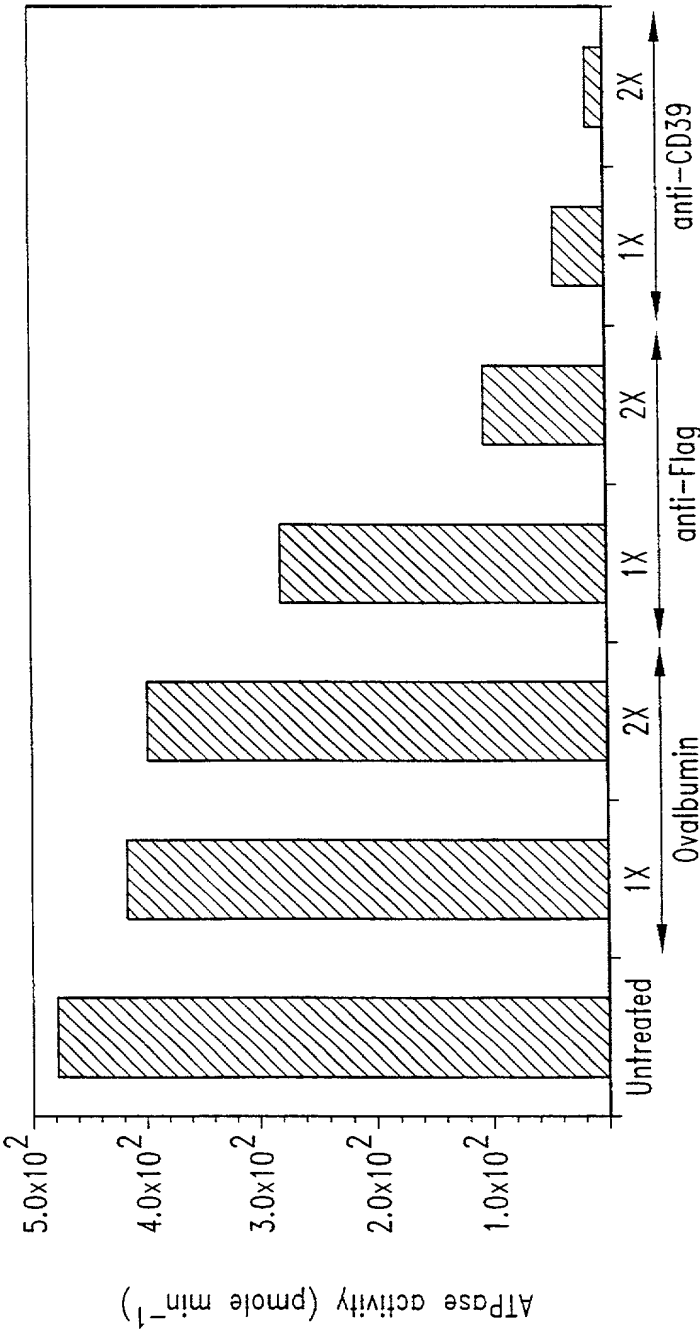


Fig. 3

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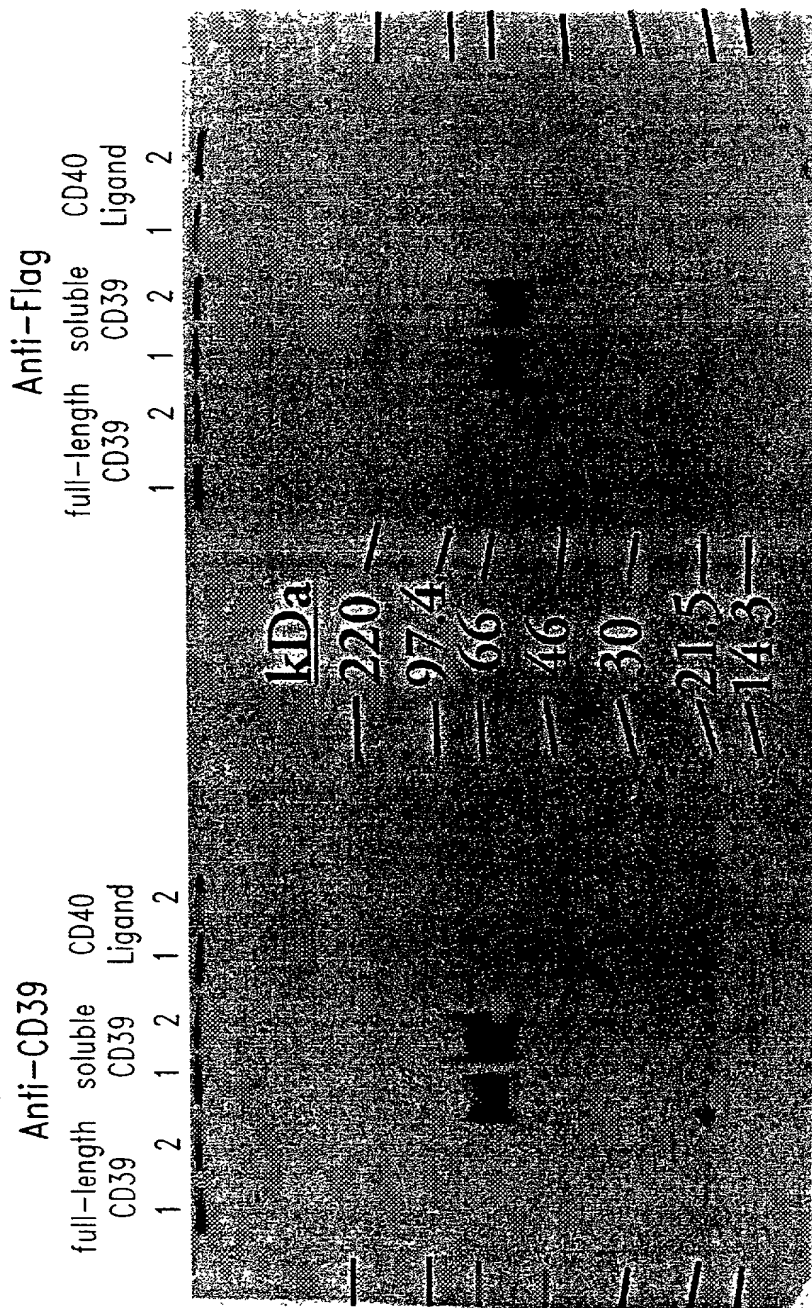
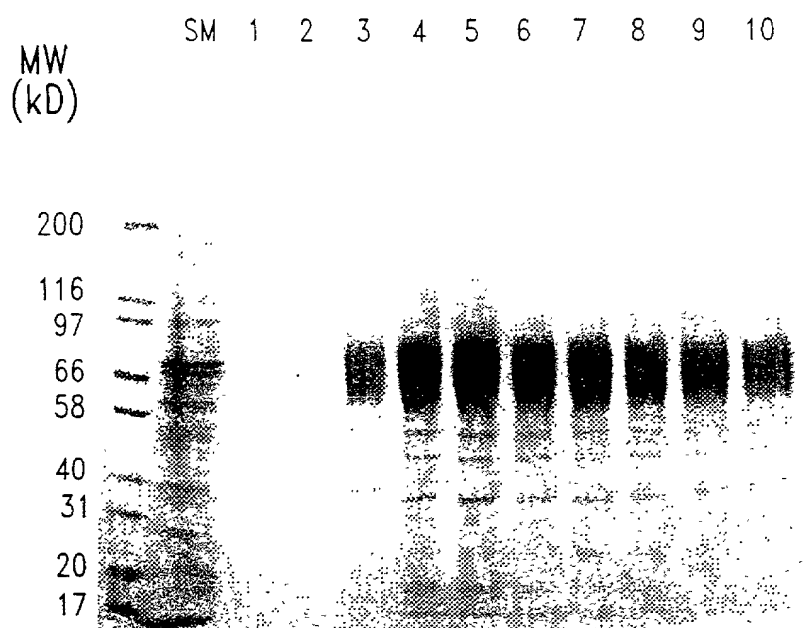
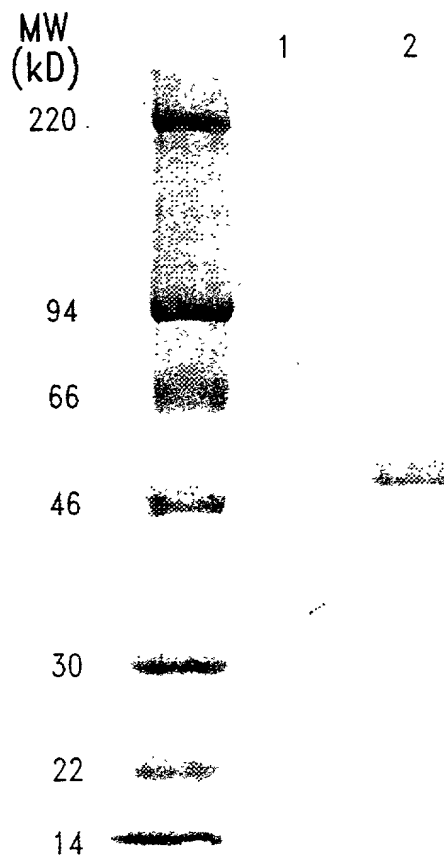
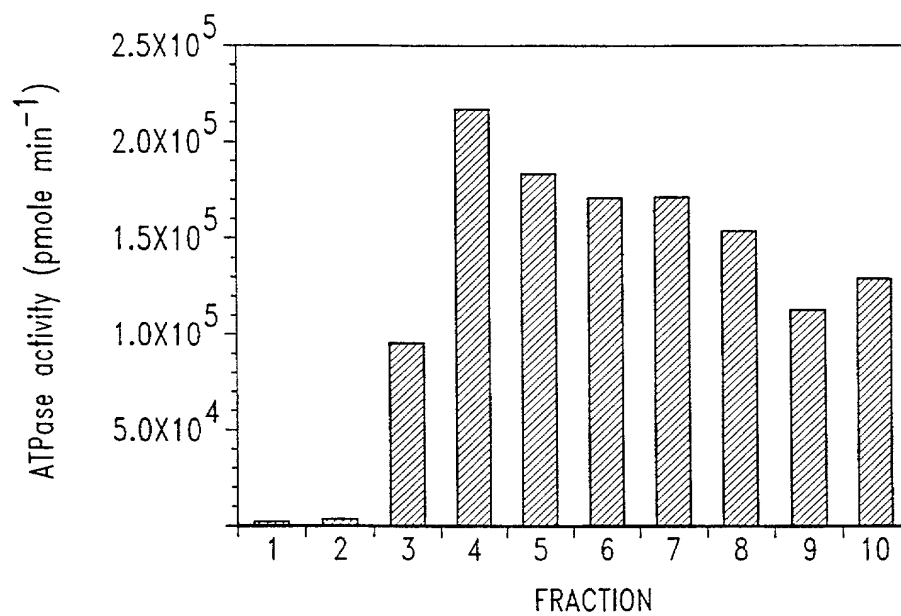


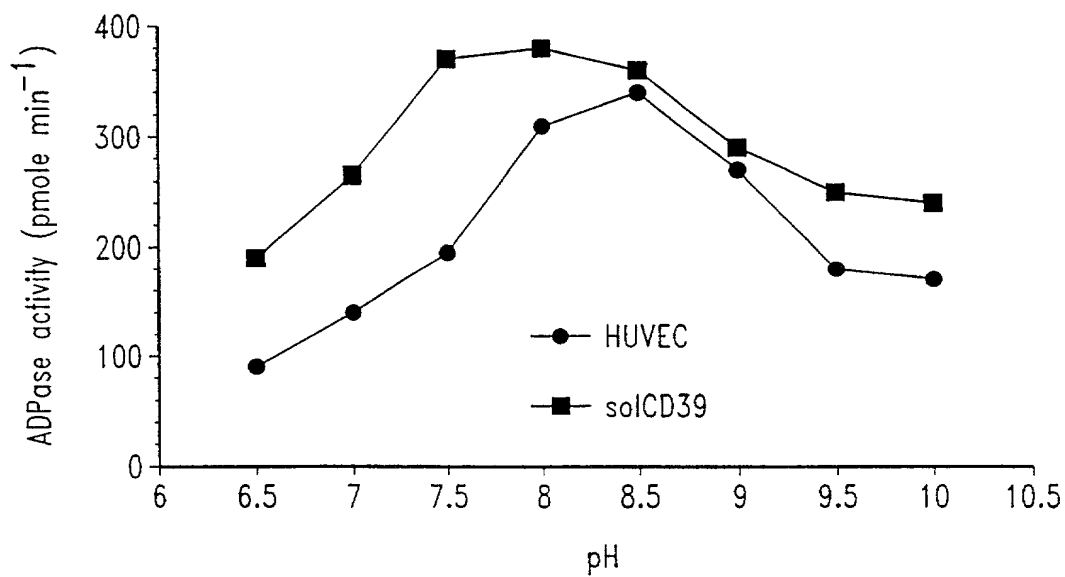
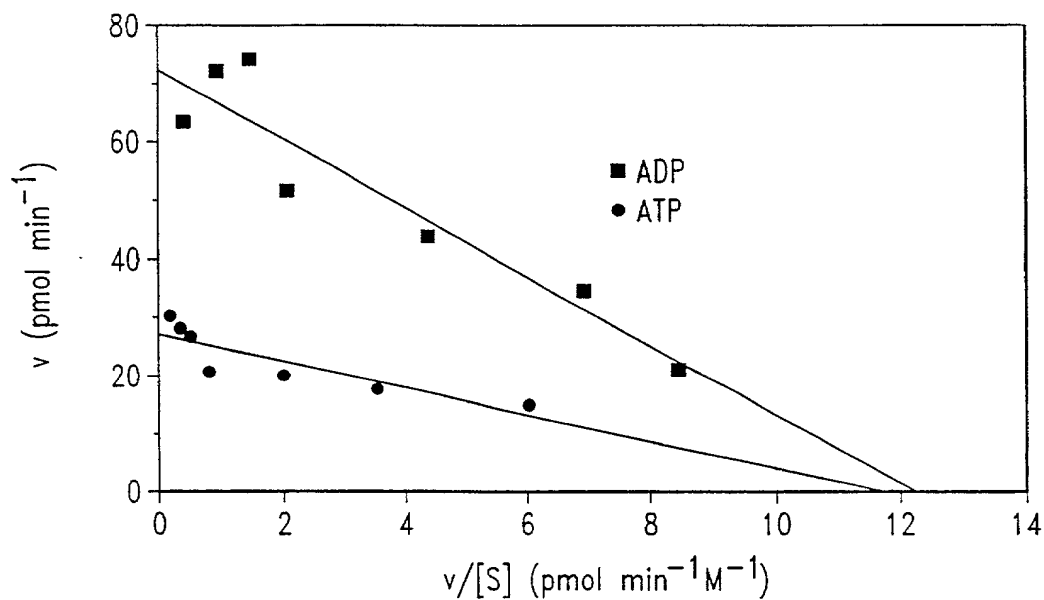
Fig. 4

*Fig. 5A**Fig. 5C*

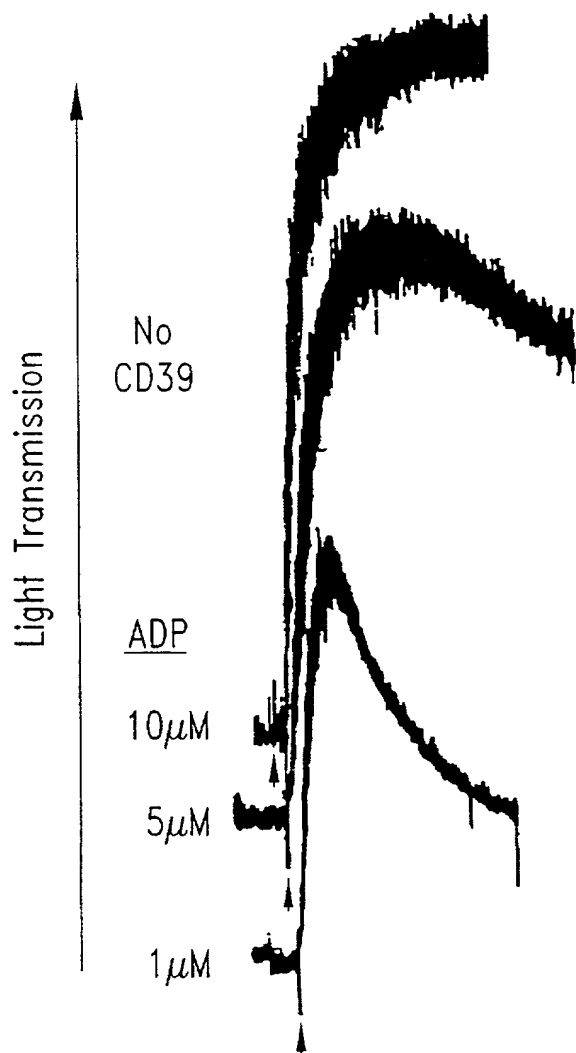
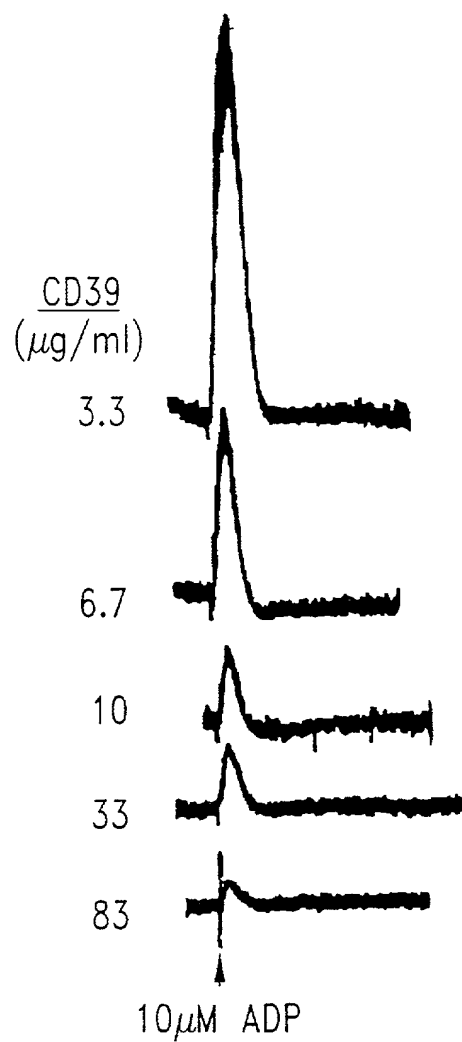
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*Fig. 5B*

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*Fig. 6A**Fig. 6B*

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*Fig. 7A**Fig. 7B*

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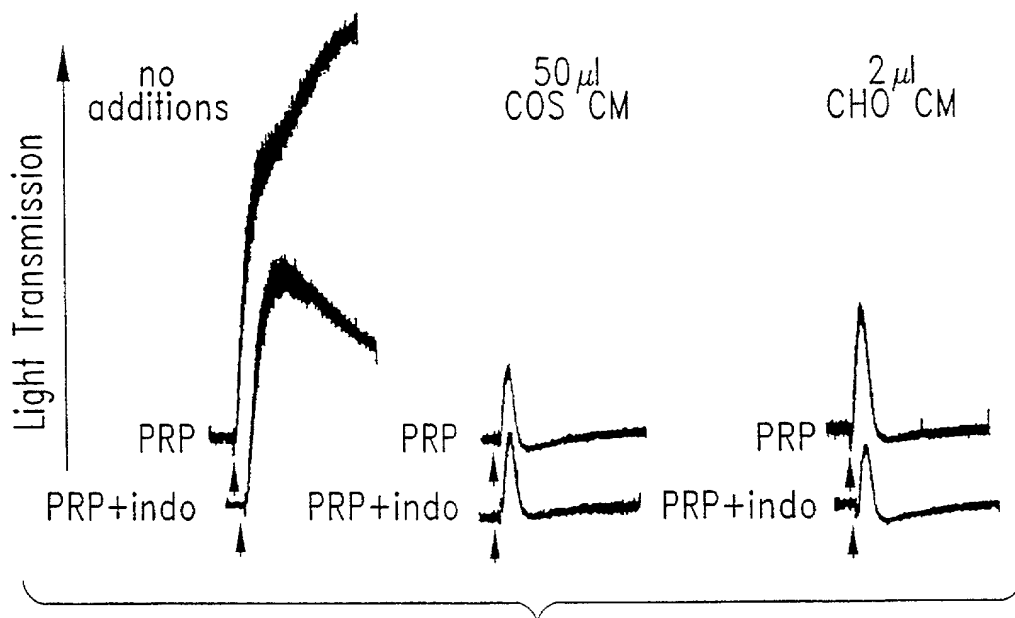


Fig. 8A

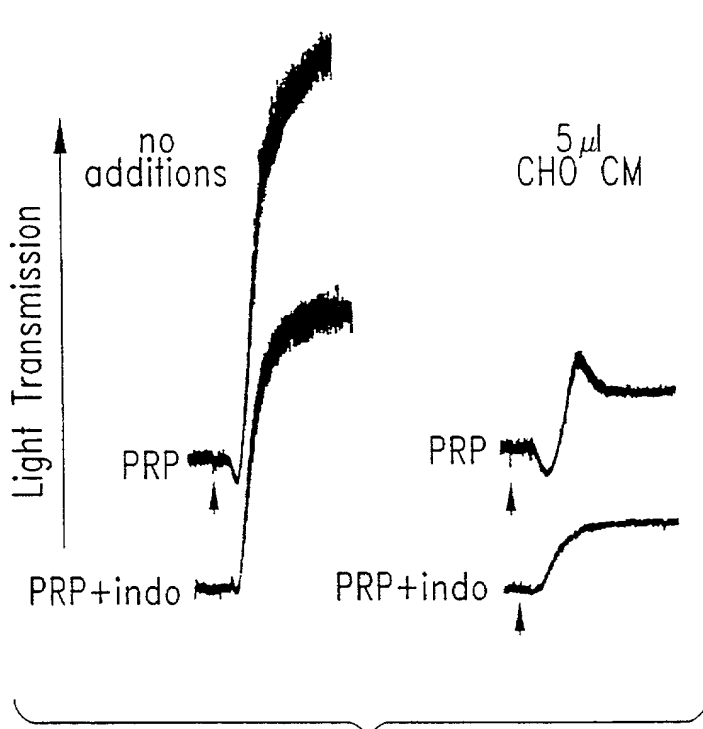


Fig. 8B

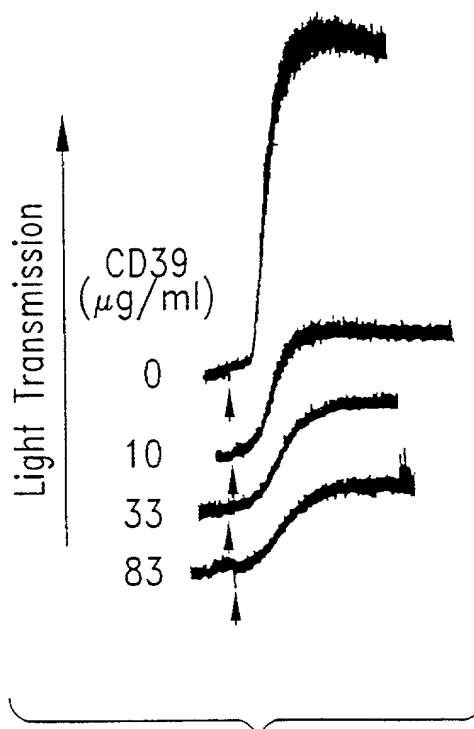
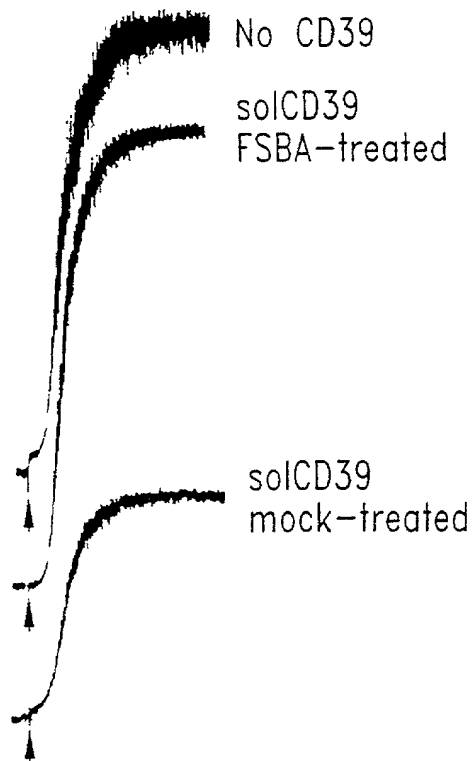
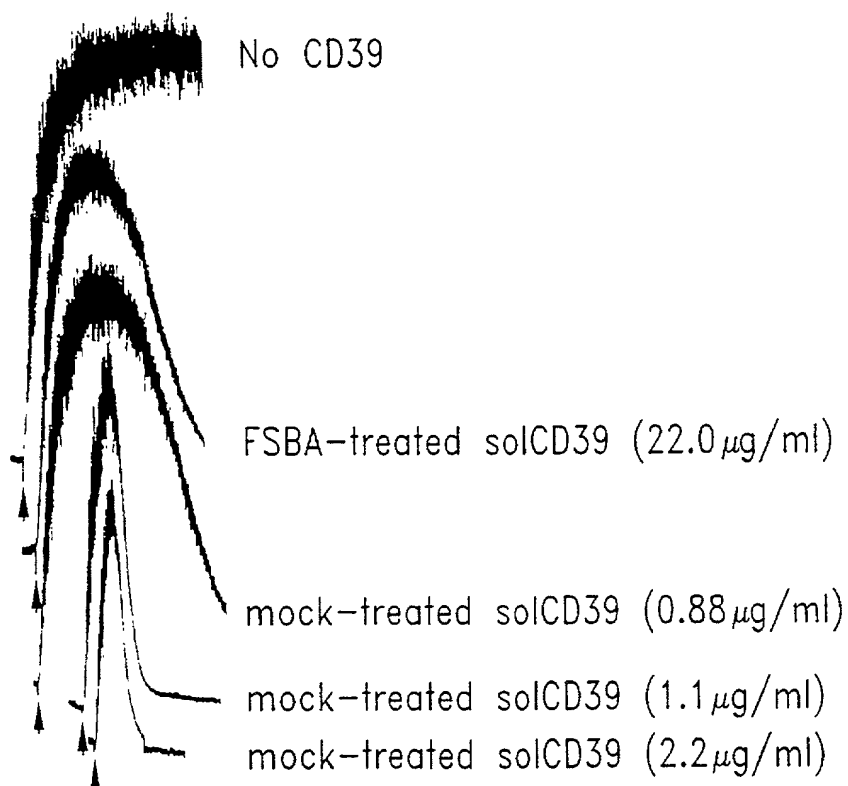
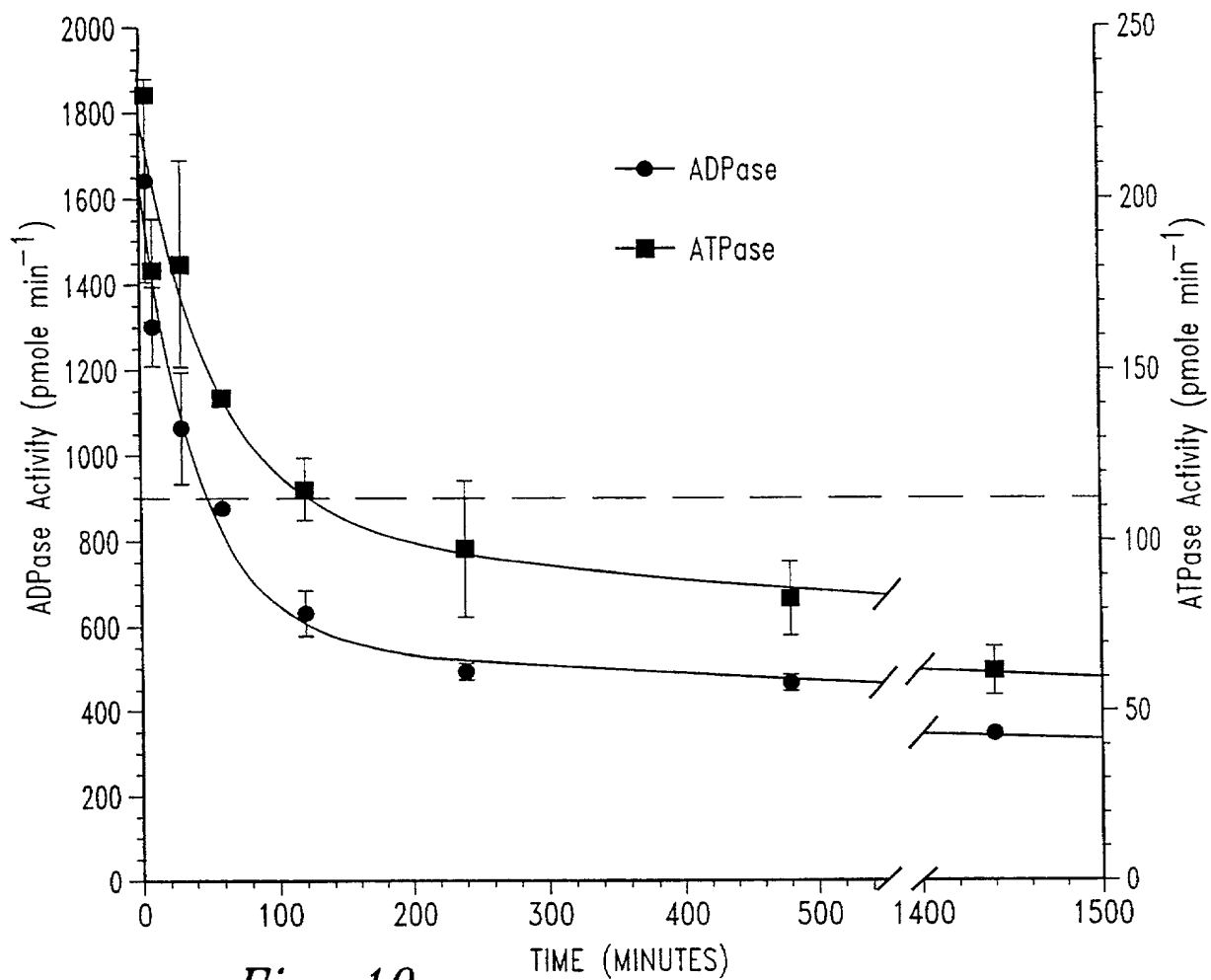
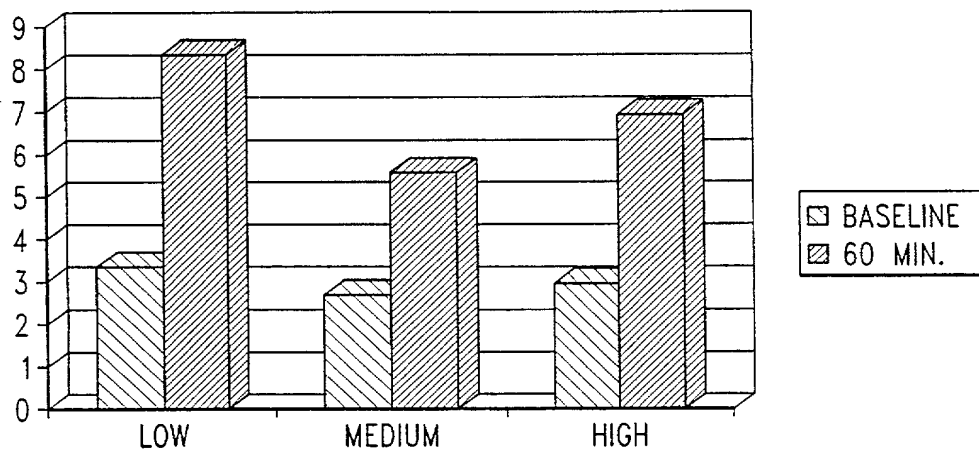


Fig. 8C

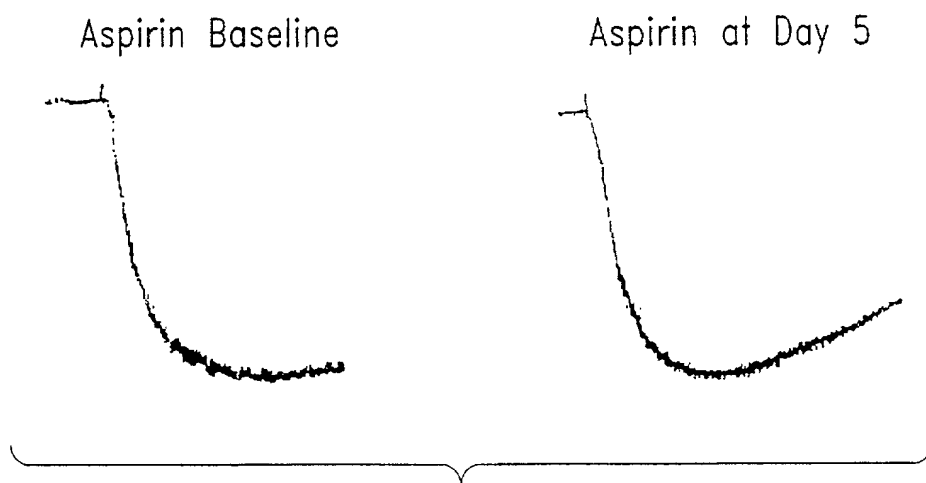
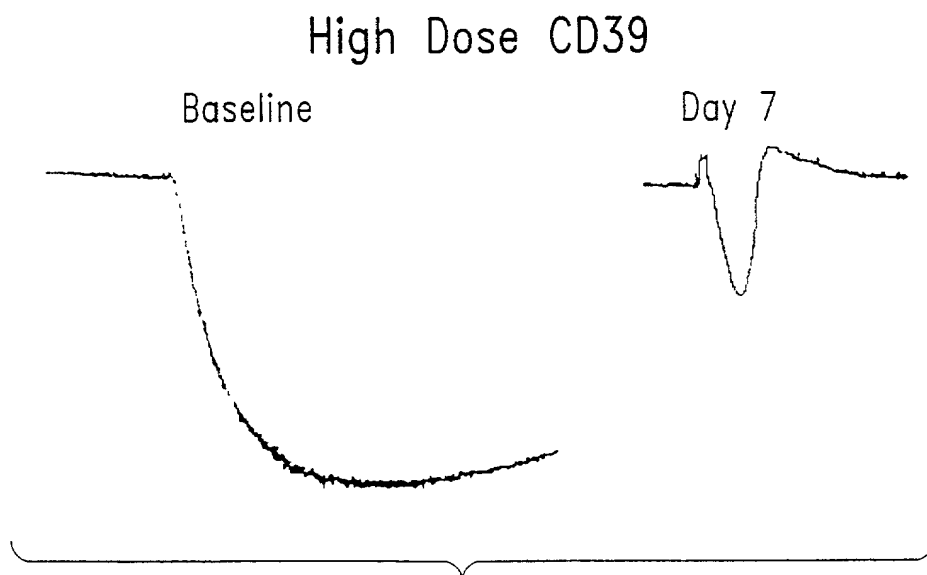
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*Fig. 9A**Fig. 9B**Fig. 9C*

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*Fig. 10**Fig. 11*

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*Fig. 12A**Fig. 12B*

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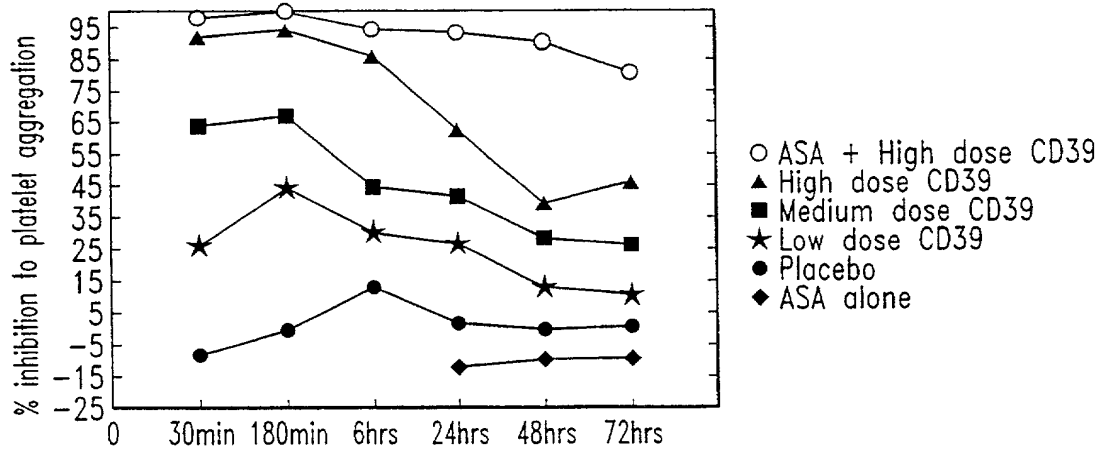


Fig. 13

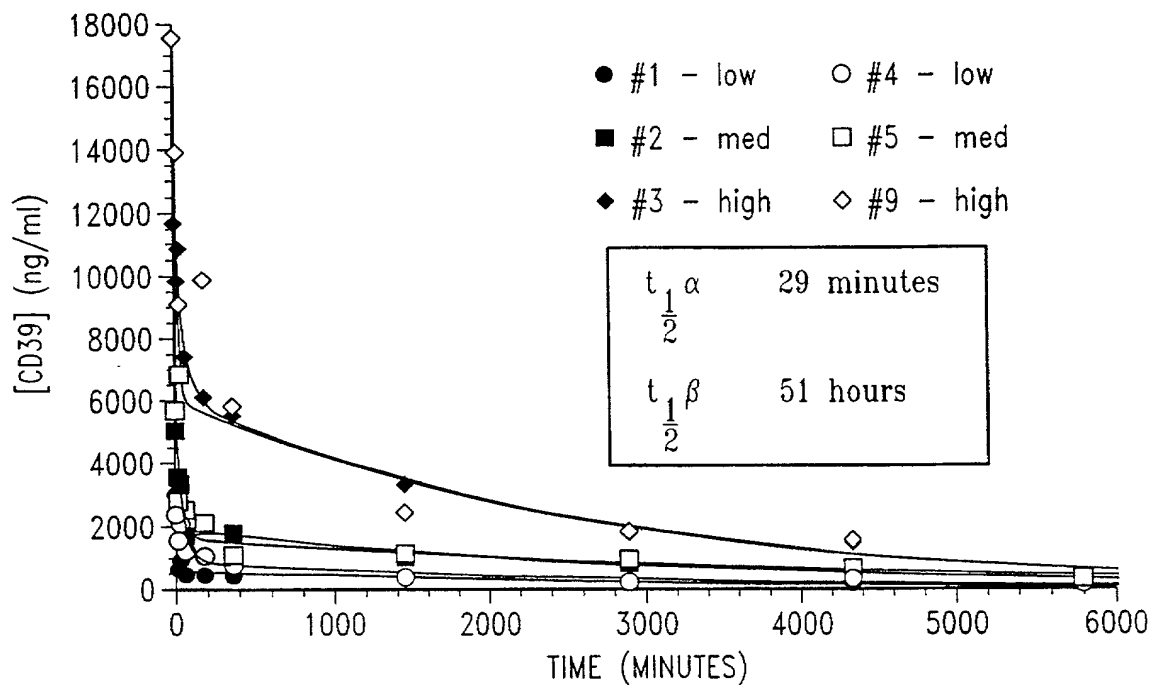
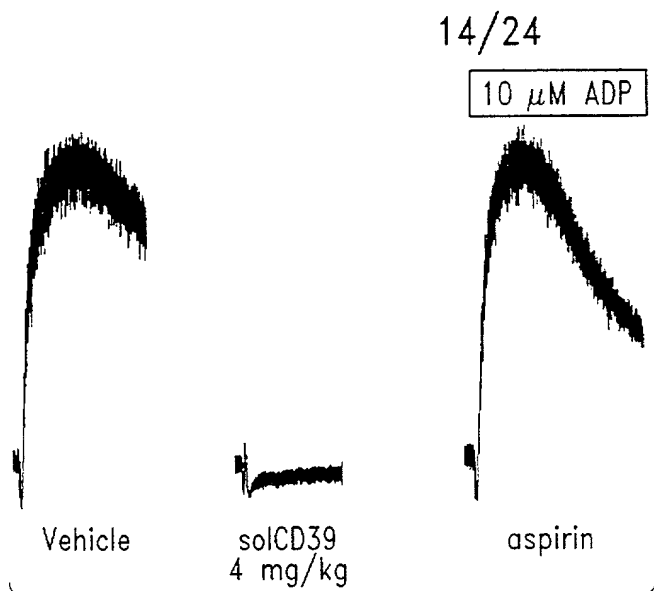
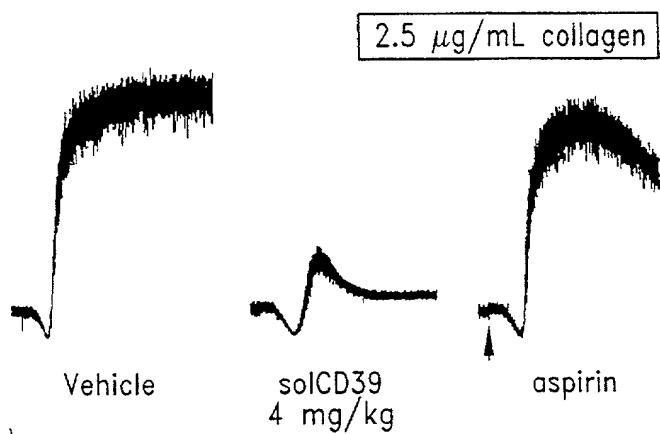
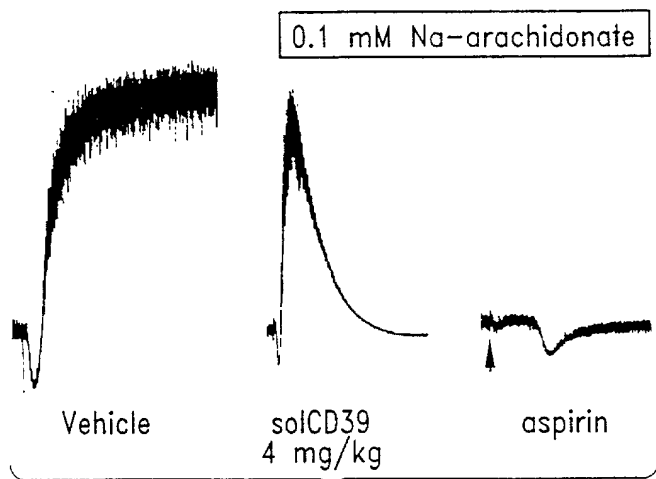
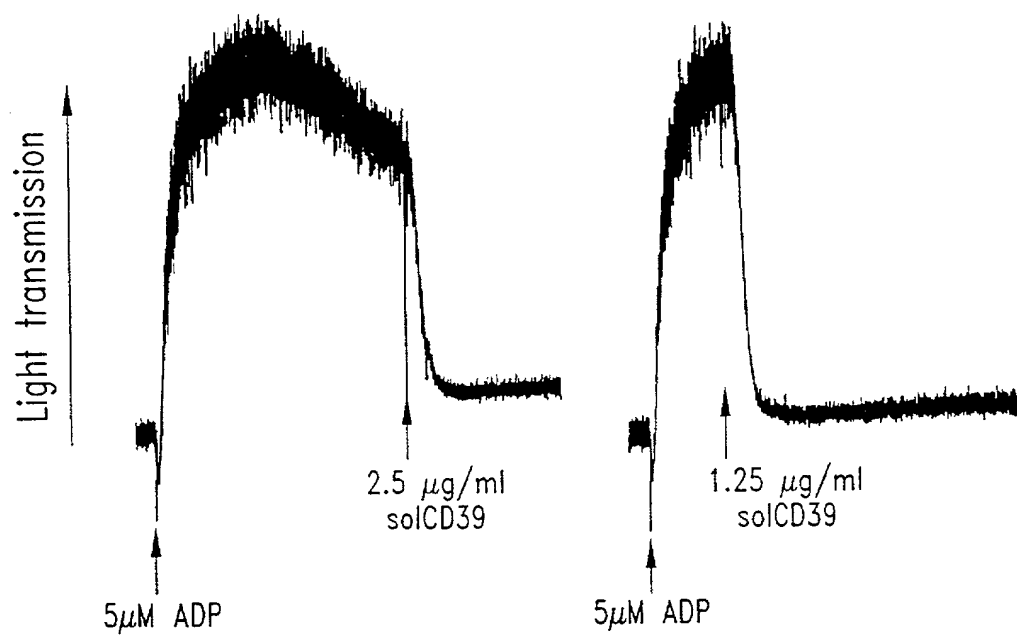
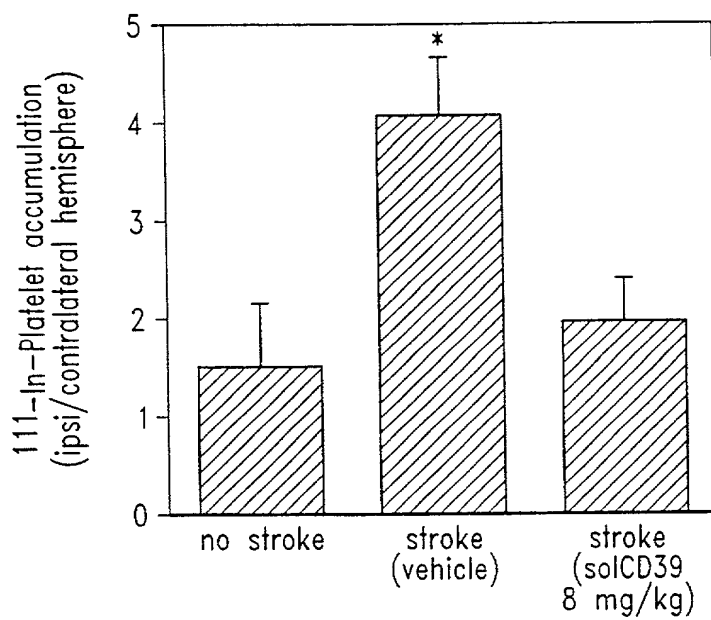


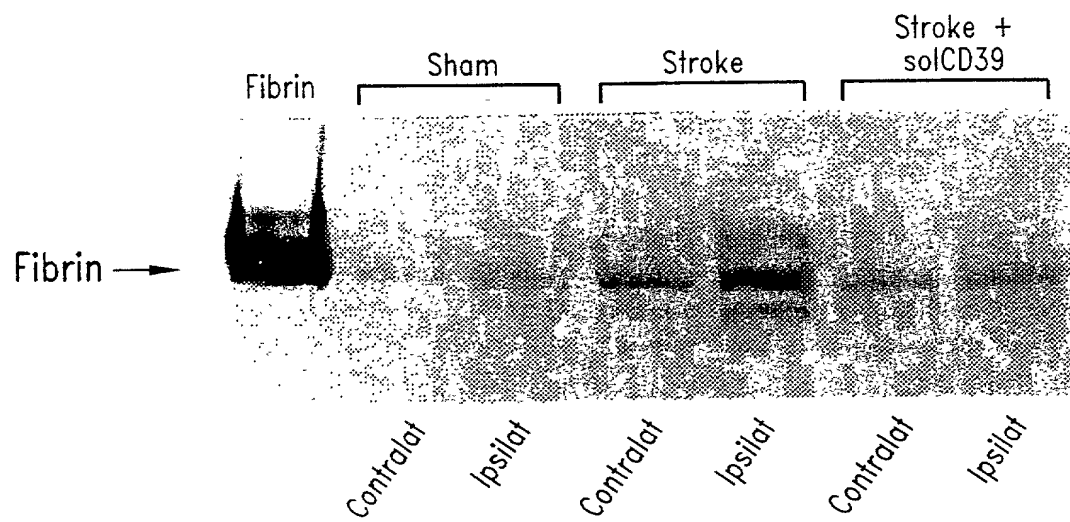
Fig. 14

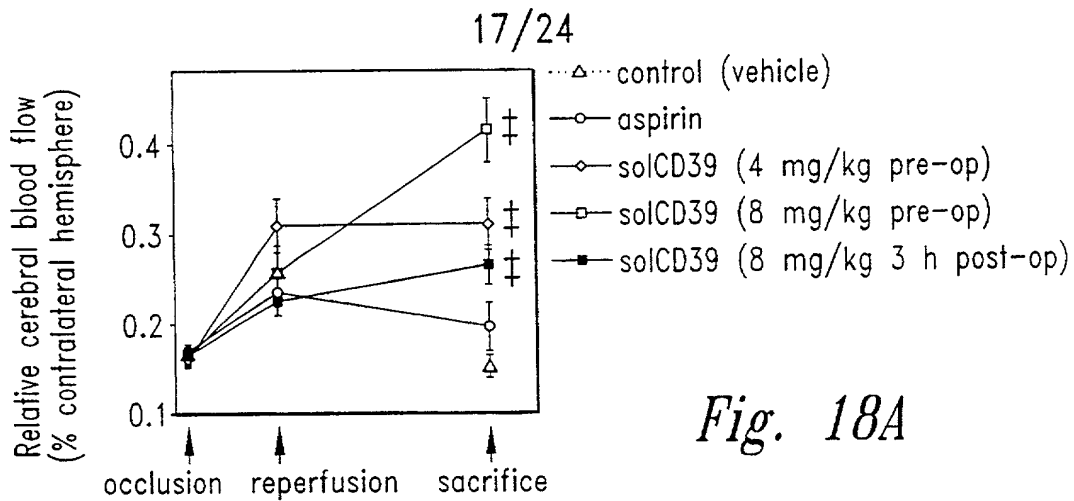
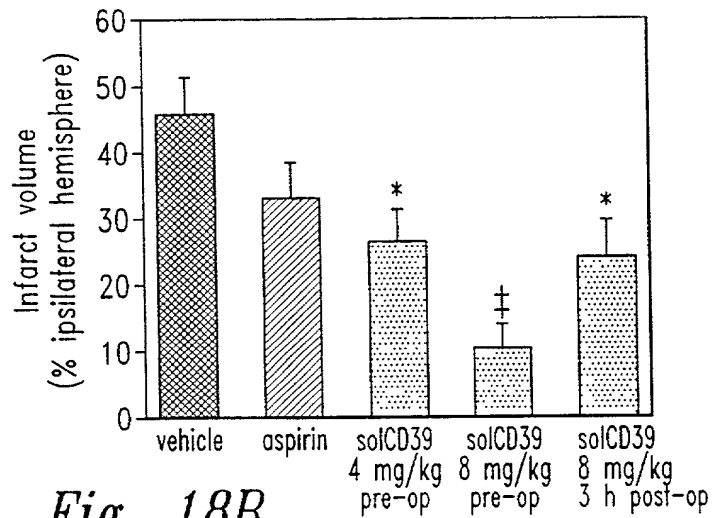
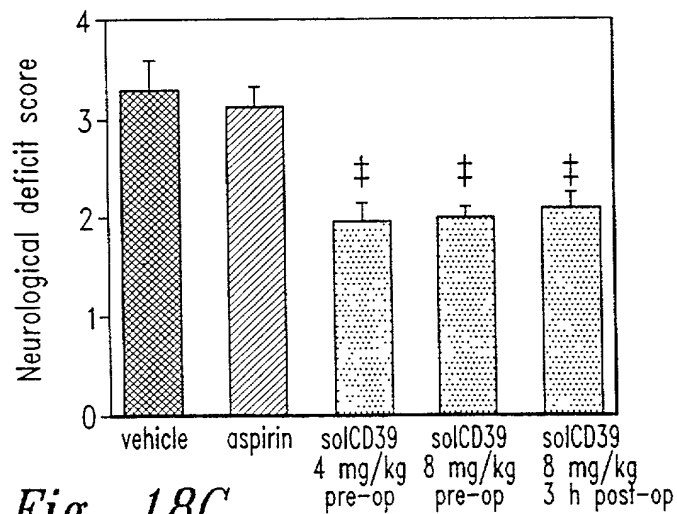
*Fig. 15A**Fig. 15B**Fig. 15C*

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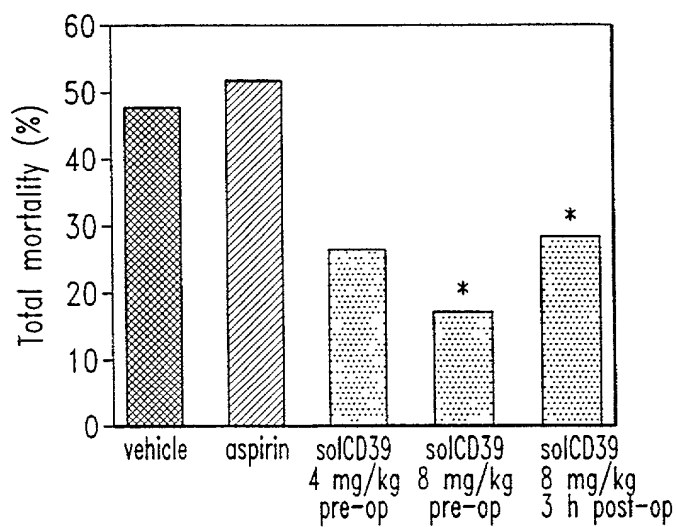
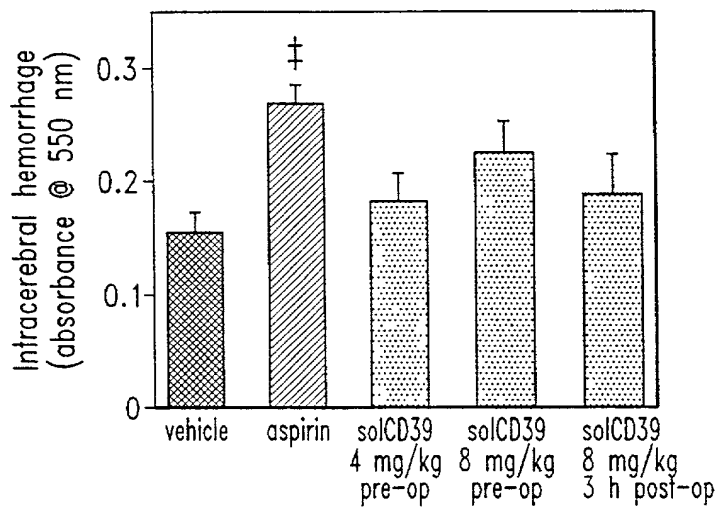
*Fig. 16**Fig. 17A*

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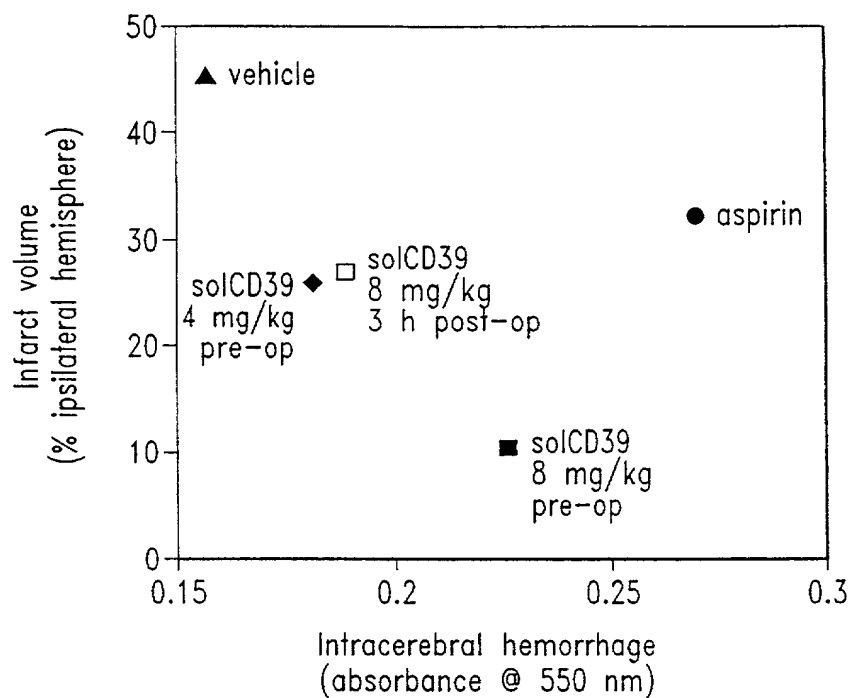
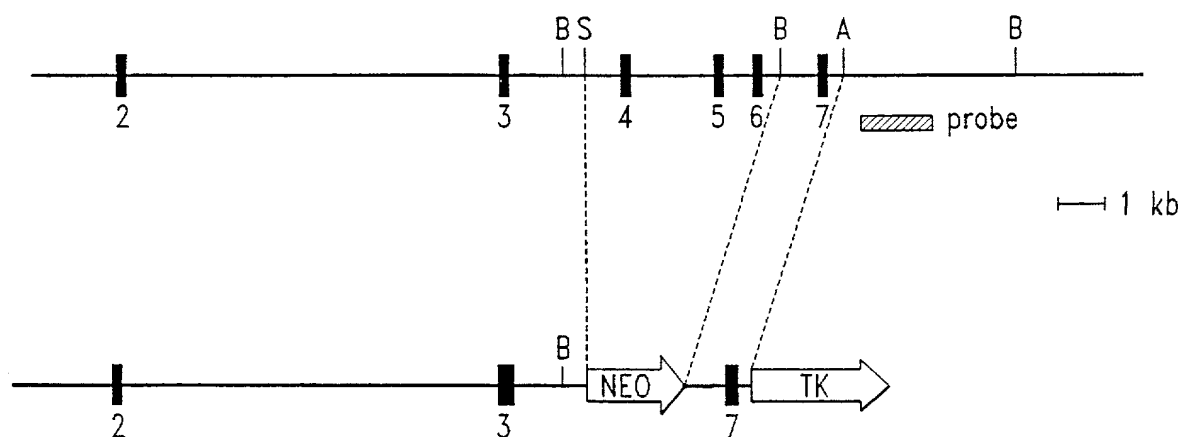
*Fig. 17B*

*Fig. 18A**Fig. 18B**Fig. 18C*

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*Fig. 18D**Fig. 18E*

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*Fig. 19**Fig. 20A*

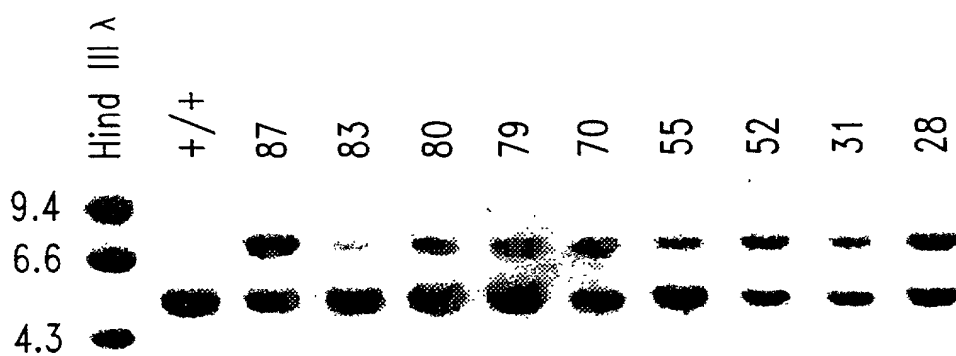
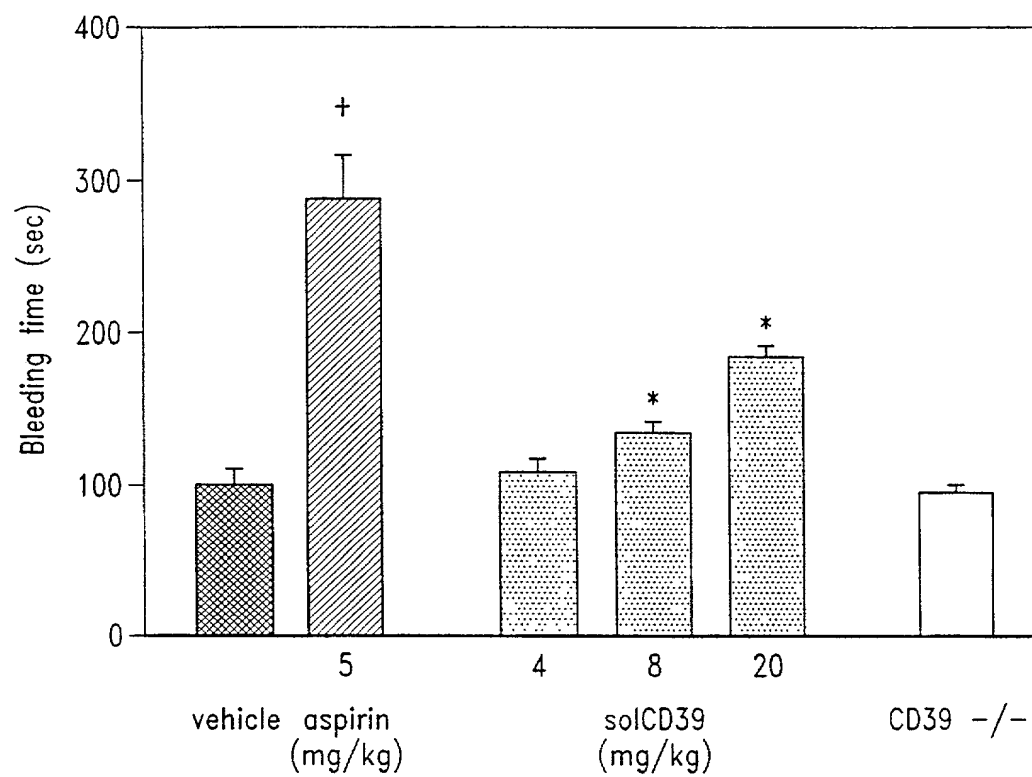
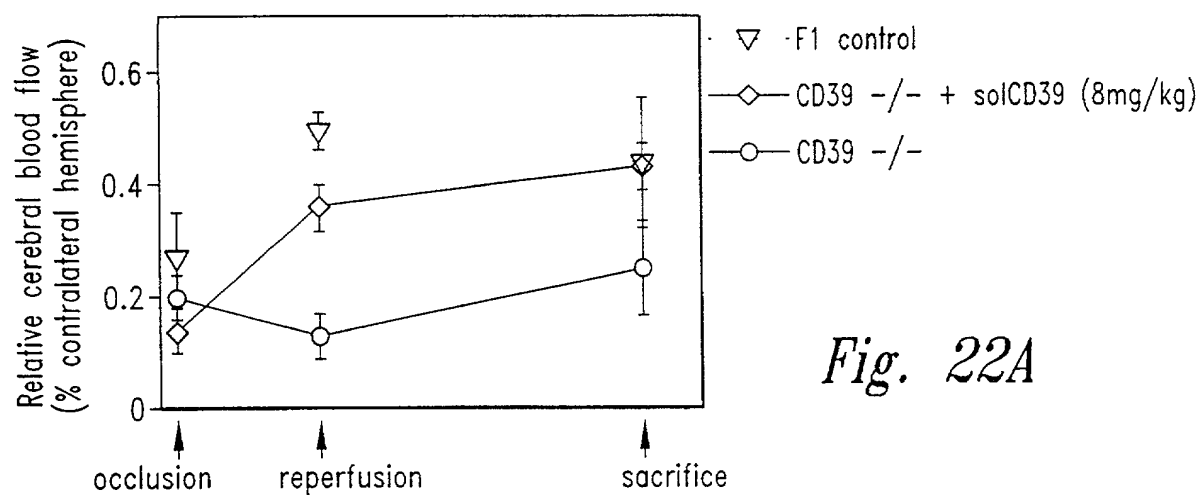
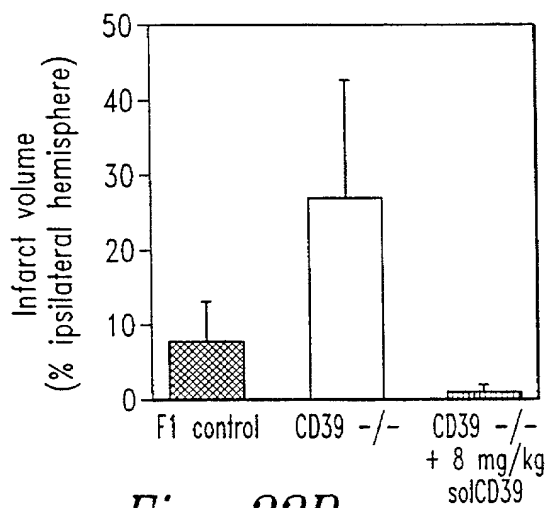
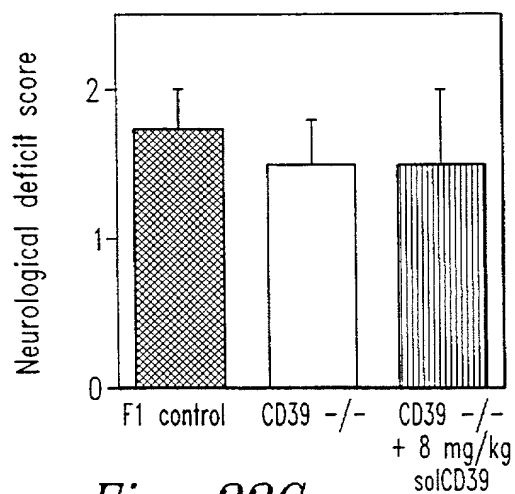


Fig. 20B

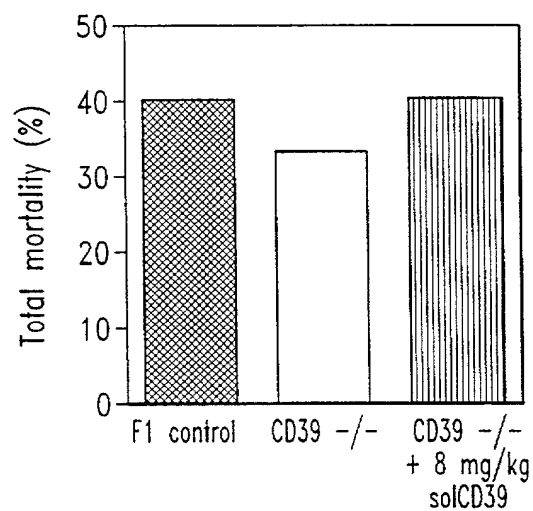
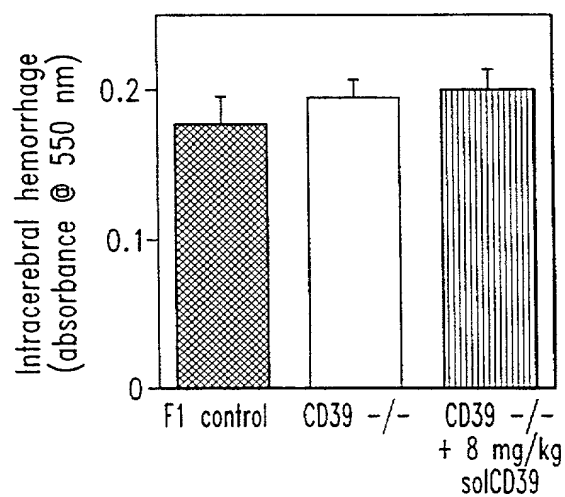
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*Fig. 21*

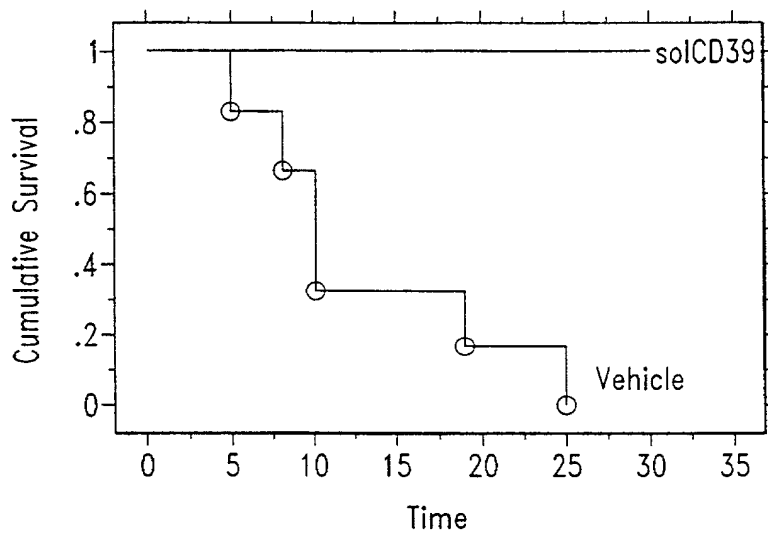
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*Fig. 22A**Fig. 22B**Fig. 22C*

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*Fig. 22D**Fig. 22E*

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*Fig. 23*

Human CD39 (amino acids 1-69 of SEQ ID NO:2)

MEDTKESNVK TFCSKNILAI LGFSSIIAVI ALLAVGLTQN KALPENVKYG IVLDAGSS...

| | | | |

MATSWGTVFF MLVVSCVCSA VSHRNQQTWF EGIFLSSMCP INVSASTLYG IMFDAGST...

Human CD39-L4 (SEQ ID NO:31)

Fig. 24

Docket No.
P23,495 USA

Declaration and Power of Attorney For Patent Application

English Language Declaration

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

METHODS OF INHIBITING PLATELET ACTIVATION AND RECRUITMENT

the specification of which

(check one)

☐ is attached hereto.

☒ was filed on 13 October 1999 (13.10.99) as United States Application No. or PCT International Application Number PCT/US99/23641 and was amended on _____

(if applicable)

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56.

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Prior Foreign Application(s)

Priority Not Claimed

(Number)

(Country)

(Day/Month/Year Filed)

☐

(Number)

(Country)

(Day/Month/Year Filed)

☐

(Number)

(Country)

(Day/Month/Year Filed)

☐

I hereby claim the benefit under 35 U.S.C. Section 119(e) of any United States provisional application(s) listed below:

<u>60/104,585</u>	<u>16 October 1998 (16.10.98)</u>
(Application Serial No.)	(Filing Date)
<u>60/107,466</u>	<u>6 November 1998 (06.11.98)</u>
(Application Serial No.)	(Filing Date)
<u>60/149,010</u>	<u>13 August 1999 (13.08.99)</u>
(Application Serial No.)	(Filing Date)

I hereby claim the benefit under 35 U. S. C. Section 120 of any United States application(s), or Section 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of 35 U.S.C. Section 112, I acknowledge the duty to disclose to the United States Patent and Trademark Office all information known to me to be material to patentability as defined in Title 37, C. F. R., Section 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of this application:

<u>PCT/US99/23641</u>	<u>13 October 1999 (13.10.99)</u>	<u>pending</u>
(Application Serial No.)	(Filing Date)	(Status)
		(patented, pending, abandoned)
<u></u>	<u></u>	<u></u>
(Application Serial No.)	(Filing Date)	(Status)
		(patented, pending, abandoned)
<u></u>	<u></u>	<u></u>
(Application Serial No.)	(Filing Date)	(Status)
		(patented, pending, abandoned)

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorney(s) and/or agent(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith. (list name and registration number)

Alexis Barron (Reg. No. 22,702)

Gregory S. Bernabeo (Reg. No. 44,032)

Peter J. Butch III (Reg. No. 32,203)

John A. Chionchio (Reg. No. 40,954)

Martin F. Savitsky (Reg. No. 29,699)

Christopher P. Dahling (registration number pending)

Stephen J. Driscoll (Reg. No. 37,564)

H. Eric Fischer (Reg. No. 46,010)

Brett T. Freeman (Reg. No. 46,709)

Gary A. Hecht (Reg. No. 36,826)

Patrick J. Kelly (Reg. No. 34,638)

Charles H. Lindrooth (Reg. No. 20,659)

Lisa B. Lane (Reg. No. 38,217)

Theodore Naccarella (Reg. No. 33,023)

Joseph F. Posillico (Reg. No. 32,290)

Mark D. Simpson (Reg. No. 32,942)

Joshua R. Slavitt (Reg. No. 40,816)

Stephen J. Weed (Reg. No. 45,202)

Gene J. Yao (Reg. No. 47,193)

Jonathan M. Dermott (Reg. No. P-48,608)

Julie K. Smith (Reg. No. 38,619)

Send Correspondence to: Patrick J. Kelly, Ph.D., Esquire
SYNNESTVEDT & LECHNER LLP
2600 Aramark Tower, 1101 Market Street
Philadelphia, Pennsylvania 19107-2950

Direct Telephone Calls to: (name and telephone number)

Patrick J. Kelly (215) 923-4466

Full name of sole or first inventor Richard B. GAYLE III	
Sole or first inventor's signature	Date
Residence 17833 149th Avenue NE, Woodinville, Washington 98072, UNITED STATES OF AMERICA	
Citizenship United States of America	
Post Office Address 17833 149th Avenue NE, Woodinville, Washington 98072, UNITED STATES OF AMERICA	

Full name of second inventor, if any Aaron J. MARCUS	
Second inventor's signature <i>x Aaron J. Marcus, M.D.</i>	Date <i>8/28/01</i>
Residence 41 Woods Lane, Scarsdale, New York 10583, UNITED STATES OF AMERICA NY	
Citizenship UNITED STATES OF AMERICA ✓	
Post Office Address 41 Woods Lane, Scarsdale, New York 10583, UNITED STATES OF AMERICA	

Full name of third inventor, if any Charles R. MALISZEWSKI	
Third inventor's signature	Date
Residence 1014 NW 120th, Seattle, Washington 98177, UNITED STATES OF AMERICA	
Citizenship UNITED STATES OF AMERICA	
Post Office Address 1014 NW 120th, Seattle, Washington 98177, UNITED STATES OF AMERICA	

Full name of fourth inventor, if any	
Fourth inventor's signature	Date
Residence	
Citizenship	
Post Office Address	

Full name of fifth inventor, if any	
Fifth inventor's signature	Date
Residence	
Citizenship	
Post Office Address	

Full name of sixth inventor, if any	
Sixth inventor's signature	Date
Residence	
Citizenship	
Post Office Address	

Docket No.
P23,495 USA

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☐ is attached hereto.

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(Number)

(Country)

(Day/Month/Year Filed)

☐

(Number)

(Country)

(Day/Month/Year Filed)

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(Day/Month/Year Filed)

☐

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(Application Serial No.)	(Filing Date)	(Status) (patented, pending, abandoned)
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Peter J. Butch III (Reg. No. 32,203)

John A. Chionchio (Reg. No. 40,954)

Martin F. Savitsky (Reg. No. 29,699)

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H. Eric Fischer (Reg. No. 46,010)

Brett T. Freeman (Reg. No. 46,709)

Gary A. Hecht (Reg. No. 36,826)

Patrick J. Kelly (Reg. No. 34,638)

Charles H. Lindrooth (Reg. No. 20,659)

Lisa B. Lane (Reg. No. 38,217)

Theodore Naccarella (Reg. No. 33,023)

Joseph F. Posillico (Reg. No. 32,290)

Mark D. Simpson (Reg. No. 32,942)

Joshua R. Slavitt (Reg. No. 40,816)

Stephen J. Weed (Reg. No. 45,202)

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Jonathan M. Dermott (Reg. No. P-48,608)

Julie K. Smith (Reg. No. 38,619)

Send Correspondence to: Patrick J. Kelly, Ph.D., Esquire
SYNNESTVEDT & LECHNER LLP
2600 Aramark Tower, 1101 Market Street
Philadelphia, Pennsylvania 19107-2950

Direct Telephone Calls to: (name and telephone number)
Patrick J. Kelly (215) 923-4466

Full name of sole or first inventor

Richard B. GAYLE III

Sole or first inventor's signature

Residence

17833 149th Avenue NE, Woodinville, Washington 98072, UNITED STATES OF AMERICA

Citizenship

United States of America ✓

Post Office Address

17833 149th Avenue NE, Woodinville, Washington 98072, UNITED STATES OF AMERICA

Date

8-21-01

Full name of second inventor, if any

Aaron J. MARCUS

Second inventor's signature

Date

Residence

41 Woods Lane, Scarsdale, New York 10583, UNITED STATES OF AMERICA

Citizenship

UNITED STATES OF AMERICA

Post Office Address

41 Woods Lane, Scarsdale, New York 10583, UNITED STATES OF AMERICA

3-00
Full name of third inventor, if any

Charles R. MALISZEWSKI

Third inventor's signature

CR Maliszewski

Date

8-21-01

Residence

1014 NW 120th, Seattle, Washington 98177, UNITED STATES OF AMERICA

WA

Citizenship

UNITED STATES OF AMERICA

Post Office Address

1014 NW 120th, Seattle, Washington 98177, UNITED STATES OF AMERICA

Full name of fourth inventor, if any

Fourth inventor's signature

Date

Residence

Citizenship

Post Office Address

Full name of fifth inventor, if any

Fifth inventor's signature

Date

Residence

Citizenship

Post Office Address

Full name of sixth inventor, if any

Sixth inventor's signature

Date

Residence

Citizenship

Post Office Address

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Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	
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aag	aga	ttt	gag	atg	act	ctt	cca	ttc	cag	cag	ttt	gaa	atc	cag	ggg	1020
Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	
		305					310					315				

att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac	1068
Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn	
320 325 330	
acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg	1116
Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu	
335 340 345 350	
cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg	1164
Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val	
355 360 365	
atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg	1212
Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val	
370 375 380	
act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa	1260
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys	
385 390 395	
aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt	1308
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe	
400 405 410	
tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca	1356
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr	
415 420 425 430	
gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc	1404
Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser	
435 440 445	
gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc	1452
Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile	
450 455 460	
cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc	1500
Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val	
465 470 475	
ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata	1548
Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile	
480 485 490	
ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta	1596
Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val	
495 500 505 510	
tag	1599

<210> 2

<211> 510

<212> PRT

<213> Homo sapiens

<400> 2

Met	Glu	Asp	Thr	Lys	Glu	Ser	Asn	Val	Lys	Thr	Phe	Cys	Ser	Lys	Asn
1				5					10						15

Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
 20 25 30
 Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
 35 40 45
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50 55 60
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
 65 70 75 80
 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
 85 90 95
 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
 100 105 110
 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
 115 120 125
 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
 130 135 140
 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
 145 150 155 160
 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
 165 170 175
 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
 180 185 190
 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
 195 200 205
 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
 210 215 220
 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
 225 230 235 240
 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
 245 250 255
 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
 260 265 270
 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
 275 280 285
 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
 290 295 300
 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
 305 310 315 320
 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
 325 330 335

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Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
465 470 475 480

Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
485 490 495

Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
500 505 510

<210> 3

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 3

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln

				85					90					95			
Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala		
			100					105					110				
Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu		
		115					120					125					
Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu		
	130					135					140						
Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro		
145					150					155					160		
Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala		
				165					170					175			
Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys		
			180					185					190				
Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr		
		195					200					205					
Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val		
	210					215					220						
Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg		
225					230					235					240		
Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr		
				245					250					255			
Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val		
			260					265					270				
Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys		
		275					280					285					
Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg		
	290					295					300						
Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly		
305					310					315					320		
Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser		
				325					330					335			
Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro		
			340					345					350				
Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys		
		355					360					365					
Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu		
	370					375					380						
Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser		
385					390					395					400		
Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly		

405 410 415
 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
 420 425 430
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
 435 440 445
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
 450 455 460
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

<210> 4

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<220>

<221> VARIANT

<222> (39)

<223> Any amino acid, preferably Cys or Ser

<400> 4

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
 1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
 20 25 30

Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu
 35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
 50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
 65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
 85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
 100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
 115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
 130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
 145 150 155 160

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Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165 170 175
Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180 185 190
Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205
Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210 215 220
Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225 230 235 240
Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245 250 255
Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260 265 270
Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
275 280 285
Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
290 295 300
Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305 310 315 320
Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
325 330 335
Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
340 345 350
Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
355 360 365
Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380
Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400
Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415
Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430
Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445
Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
450 455 460
Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470 475

<210> 5
 <211> 1365
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<220>
 <221> CDS
 <222> (1)..(1362)

<400> 5
 gca cct act tca agt tct aca aag aaa aca cag cta act agt tca acc 48
 Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
 1 5 10 15

cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg gat 96
 Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
 20 25 30

gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca gaa 144
 Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
 35 40 45

aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg gtt 192
 Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
 50 55 60

aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata ggc 240
 Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
 65 70 75 80

att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca agg 288
 Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
 85 90 95

tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc atg 336
 Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
 100 105 110

cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg gat 384
 Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
 115 120 125

gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt gcc 432
 Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
 130 135 140

agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act atc 480
 Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
 145 150 155 160

aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc ata 528
 Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile
 165 170 175

gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac ctt 576

Val	Pro	Tyr	Glu 180	Thr	Asn	Asn	Gln	Glu 185	Thr	Phe	Gly	Ala	Leu 190	Asp	Leu	
ggg Gly	gga Gly	gcc Ala 195	tct Ser	aca Thr	caa Gln	gtc Val	act Thr 200	ttt Phe	gta Val	ccc Pro	caa Gln	aac Asn 205	cag Gln	act Thr	atc Ile	624
gag Glu	tcc Ser 210	cca Pro	gat Asp	aat Asn	gct Ala	ctg Leu 215	caa Gln	ttt Phe	cgc Arg	ctc Leu	tat Tyr 220	ggc Gly	aag Lys	gac Asp	tac Tyr	672
aat Asn 225	gtc Val	tac Tyr	aca Thr	cat His	agc Ser 230	ttc Phe	ttg Leu	tgc Cys	tat Tyr	ggg Gly 235	aag Lys	gat Asp	cag Gln	gca Ala	ctc Leu 240	720
tgg Trp	cag Gln	aaa Lys	ctg Leu	gcc Ala 245	aag Lys	gac Asp	att Ile	cag Gln	gtt Val 250	gca Ala	agt Ser	aat Asn	gaa Glu	att Ile 255	ctc Leu	768
agg Arg	gac Asp	cca Pro	tgc Cys 260	ttt Phe	cat His	cct Pro	gga Gly	tat Tyr 265	aag Lys	aag Lys	gta Val	gtg Val	aac Asn 270	gta Val	agt Ser	816
gac Asp	ctt Leu	tac Tyr 275	aag Lys	acc Thr	ccc Pro	tgc Cys	acc Thr 280	aag Lys	aga Arg	ttt Phe	gag Glu	atg Met 285	act Thr	ctt Leu	cca Pro	864
ttc Phe	cag Gln 290	cag Gln	ttt Phe	gaa Glu	atc Ile	cag Gln 295	ggg Gly	att Ile	gga Gly	aac Asn	tat Tyr 300	caa Gln	caa Gln	tgc Cys	cat His	912
caa Gln 305	agc Ser	atc Ile	ctg Leu	gag Glu	ctc Leu 310	ttc Phe	aac Asn	acc Thr	agt Ser	tac Tyr 315	tgc Cys	cct Pro	tac Tyr	tcc Ser	cag Gln 320	960
tgt Cys	gcc Ala	ttc Phe	aat Asn	ggg Gly 325	att Ile	ttc Phe	ttg Leu	cca Pro	cca Pro 330	ctc Leu	cag Gln	ggg Gly	gat Asp	ttt Phe 335	ggg Gly	1008
gca Ala	ttt Phe	tca Ser	gct Ala 340	ttt Phe	tac Tyr	ttt Phe	gtg Val 345	atg Met	aag Lys	ttt Phe	tta Leu	aac Asn	ttg Leu 350	aca Thr	tca Ser	1056
gag Glu	aaa Lys	gtc Val 355	tct Ser	cag Gln	gaa Glu	aag Lys	gtg Val 360	act Thr	gag Glu	atg Met	atg Met	aaa Lys 365	aag Lys	ttc Phe	tgt Cys	1104
gct Ala	cag Gln	cct Pro	tgg Trp	gag Glu	gag Glu	ata Ile 375	aaa Lys	aca Thr	tct Ser	tac Tyr	gct Ala 380	gga Gly	gta Val	aag Lys	gag Glu	1152
aag Lys 385	tac Tyr	ctg Leu	agt Ser	gaa Glu	tac Tyr 390	tgc Cys	ttt Phe	tct Ser	ggg Gly	acc Thr 395	tac Tyr	att Ile	ctc Leu	tcc Ser	ctc Leu 400	1200
ctt Leu	ctg Leu	caa Gln	ggc Gly	tat Tyr 405	cat His	ttc Phe	aca Thr	gct Ala	gat Asp 410	tcc Ser	tgg Trp	gag Glu	cac His	atc Ile 415	cat His	1248
ttc	att	ggc	aag	atc	cag	ggc	agc	gac	gcc	ggc	tgg	act	ttg	ggc	tac	1296

Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr
 210 215 220
 Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu
 225 230 235 240
 Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu
 245 250 255
 Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser
 260 265 270
 Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro
 275 280 285
 Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His
 290 295 300
 Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln
 305 310 315 320
 Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly
 325 330 335
 Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser
 340 345 350
 Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
 355 360 365
 Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu
 370 375 380
 Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
 385 390 395 400
 Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
 405 410 415
 Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr
 420 425 430
 Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr
 435 440 445
 Pro Leu Ser His Ser Thr
 450

<210> 7

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<220>

<221> CDS

<222> (1)..(1434)

<400> 7

atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta	48
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu	
1 5 10 15	
agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag	96
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys	
20 25 30	
aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac	144
Lys Thr Gln Leu Thr Ser Ser Gln Asn Lys Ala Leu Pro Glu Asn	
35 40 45	
gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta	192
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu	
50 55 60	
tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg	240
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val	
65 70 75 80	
cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt	288
His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe	
85 90 95	
gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa	336
Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu	
100 105 110	
aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt	384
Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val	
115 120 125	
tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa	432
Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu	
130 135 140	
gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac	480
Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn	
145 150 155 160	
tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa	528
Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu	
165 170 175	
ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt	576
Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser	
180 185 190	
cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag	624
Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln	
195 200 205	
gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act	672
Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr	
210 215 220	

ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa	720
Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln	
225 230 235 240	
ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg	768
Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu	
245 250 255	
tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att	816
Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile	
260 265 270	
cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga	864
Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly	
275 280 285	
tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc	912
Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr	
290 295 300	
aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt	960
Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly	
305 310 315 320	
att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac	1008
Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn	
325 330 335	
acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg	1056
Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu	
340 345 350	
cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg	1104
Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val	
355 360 365	
atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg	1152
Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val	
370 375 380	
act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa	1200
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys	
385 390 395 400	
aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt	1248
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe	
405 410 415	
tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca	1296
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr	
420 425 430	
gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc	1344
Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser	
435 440 445	
gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc	1392
Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile	
450 455 460	

cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc taa 1437
 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

<210> 8
 <211> 478
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 8
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15
 Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30
 Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn
 35 40 45
 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
 50 55 60
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
 65 70 75 80
 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
 85 90 95
 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
 100 105 110
 Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
 115 120 125
 Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
 130 135 140
 Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
 145 150 155 160
 Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
 165 170 175
 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
 180 185 190
 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
 195 200 205
 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
 210 215 220
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
 225 230 235 240

Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
245 250 255

Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
260 265 270

Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
275 280 285

Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
290 295 300

Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
305 310 315 320

Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
325 330 335

Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
340 345 350

Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
355 360 365

Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
370 375 380

Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
385 390 395 400

Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
405 410 415

Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
420 425 430

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
435 440 445

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
450 455 460

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470 475

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
signal sequence

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser

<210> 10
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 10
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 11
 <211> 43
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 11
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys
 35 40

<210> 12
 <211> 29
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 12
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys
 20 25

<210> 13
 <211> 31
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 13
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15
Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys
20 25 30

<210> 14
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 14
ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
tgtccacacc tctctccac gagcccc 87

<210> 15
<211> 87
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15
gatcggggct cgtgggagag aggtgtggac aatggttgc cagctgggat catgttggtc 60
aggttcagca tgtagcccaa agtccag 87

<210> 16
<211> 740
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (42)..(737)

<400> 16
cgtaccgct agcgtcgaca ggcctaggat atcgatacgt a gag ccc aga tct tgt 56
Glu Pro Arg Ser Cys
1 5

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggc 104
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly
10 15 20

gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg	152
Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met	
25 30 35	
atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac	200
Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His	
40 45 50	
gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg	248
Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val	
55 60 65	
cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac	296
His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr	
70 75 80 85	
cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc	344
Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly	
90 95 100	
aag gac tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atg	392
Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Met	
105 110 115	
cag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg	440
Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val	
120 125 130	
tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc	488
Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser	
135 140 145	
ctg acc tgc ctg gtc aaa ggc ttc tat ccc agg cac atc gcc gtg gag	536
Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile Ala Val Glu	
150 155 160 165	
tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc	584
Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro	
170 175 180	
gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg	632
Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val	
185 190 195	
gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg	680
Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met	
200 205 210	
cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct	728
His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser	
215 220 225	
ccg ggt aaa tga	740
Pro Gly Lys	
230	

<210> 17

<211> 232

<212> PRT

<213> Homo sapiens

<400> 17

Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
145 150 155 160

His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 18

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18

ctttccatcc tgagcaac

18

<210> 19

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19

aaaaaactag tcagaacaaa gctttgccag aaaacg

36

<210> 20

<211> 24

<212> PRT

<213> Mus sp.

<400> 20

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser
20

<210> 21

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21

ctagttctgg agactacaaa gatgacgatg acaaaaccga gaacaa

46

<210> 22

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 22

agctttgttc tgggttttgt catcgatc tttgtagtct ccagaa

46

<210> 23

<211> 89

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 23

ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60
tgtccacacc tctctccac tccacctaa 89

<210> 24

<211> 89

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 24

ggccttaggt ggagtgagg agaggtgtgg acaatggttg ctcagctggg atcatgttgg 60
tcaggttcag catgtagccc aaagtccag 89

<210> 25

<211> 1464

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1461)

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 25

atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta	48
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu	
1 5 10 15	
agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag	96
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys	
20 25 30	
aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa	144
Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys	
35 40 45	
acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg	192
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu	
50 55 60	
gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca	240
Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala	
65 70 75 80	
gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg	288

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
85 90 95

gtt aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata 336
Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
100 105 110

ggc att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca 384
Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
115 120 125

agg tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc 432
Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
130 135 140

atg cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg 480
Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
145 150 155 160

gat gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt 528
Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
165 170 175

gcc agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act 576
Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
180 185 190

atc aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc 624
Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
195 200 205

ata gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac 672
Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
210 215 220

ctt ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act 720
Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr
225 230 235 240

atc gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac 768
Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp
245 250 255

tac aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca 816
Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
260 265 270

ctc tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att 864
Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
275 280 285

ctc agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta 912
Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
290 295 300

agt gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt 960
Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
305 310 315 320

cca ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc 1008

Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys	
				325					330					335		
cat	caa	agc	atc	ctg	gag	ctc	ttc	aac	acc	agt	tac	tgc	cct	tac	tcc	1056
His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	
			340					345					350			
cag	tgt	gcc	ttc	aat	ggg	att	ttc	ttg	cca	cca	ctc	cag	ggg	gat	ttt	1104
Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe	
		355					360					365				
ggg	gca	ttt	tca	gct	ttt	tac	ttt	gtg	atg	aag	ttt	tta	aac	ttg	aca	1152
Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys	Phe	Leu	Asn	Leu	Thr	
	370					375					380					
tca	gag	aaa	gtc	tct	cag	gaa	aag	gtg	act	gag	atg	atg	aaa	aag	ttc	1200
Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu	Met	Met	Lys	Lys	Phe	
	385				390					395					400	
tgt	gct	cag	cct	tgg	gag	gag	ata	aaa	aca	tct	tac	gct	gga	gta	aag	1248
Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser	Tyr	Ala	Gly	Val	Lys	
			405						410					415		
gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	tct	ggt	acc	tac	att	ctc	tcc	1296
Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly	Thr	Tyr	Ile	Leu	Ser	
			420				425						430			
ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	gct	gat	tcc	tgg	gag	cac	atc	1344
Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp	Ser	Trp	Glu	His	Ile	
		435					440					445				
cat	ttc	att	ggc	aag	atc	cag	ggc	agc	gac	gcc	ggc	tgg	act	ttg	ggc	1392
His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala	Gly	Trp	Thr	Leu	Gly	
	450					455				460						
tac	atg	ctg	aac	ctg	acc	aac	atg	atc	cca	gct	gag	caa	cca	ttg	tcc	1440
Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	Pro	Ala	Glu	Gln	Pro	Leu	Ser	
	465				470				475					480		
aca	cct	ctc	tcc	cac	tcc	acc	taa									1464
Thr	Pro	Leu	Ser	His	Ser	Thr										
				485												

<210> 26

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 26

Met	Ala	Leu	Trp	Ile	Asp	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu
1				5				10					15		

Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys
			20					25					30		

Lys	Thr	Gln	Leu	Thr	Ser	Ser	Gly	Asp	Tyr	Lys	Asp	Asp	Asp	Lys	
		35					40				45				
Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	Val	Lys	Tyr	Gly	Ile	Val	Leu
		50				55				60					
Asp	Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile	Tyr	Lys	Trp	Pro	Ala
65					70					75					80
Glu	Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg
				85					90					95	
Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile
			100					105					110		
Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro
		115				120						125			
Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly
		130				135					140				
Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu
145					150					155					160
Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly
				165					170					175	
Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr
			180					185					190		
Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser
		195					200					205			
Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp
		210				215					220				
Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr
225					230					235					240
Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp
				245					250					255	
Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala
			260					265					270		
Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile
		275					280					285			
Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys	Lys	Val	Val	Asn	Val
		290				295					300				
Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	Lys	Arg	Phe	Glu	Met	Thr	Leu
305					310					315					320
Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys
				325					330					335	
His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser
			340					345					350		

Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe
355 360 365

Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr
370 375 380

Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe
385 390 395 400

Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys
405 410 415

Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser
420 425 430

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
435 440 445

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
450 455 460

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
465 470 475 480

Thr Pro Leu Ser His Ser Thr
485

<210> 27

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 27

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro
20 25 30

Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr
35 40 45

Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly
50 55 60

Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser
65 70 75 80

Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys
85 90 95

Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr
100 105 110

Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu
 115 120 125
 Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu
 130 135 140
 Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln
 145 150 155 160
 Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys
 165 170 175
 Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn
 180 185 190
 Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln
 195 200 205
 Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala
 210 215 220
 Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser
 225 230 235 240
 Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys
 245 250 255
 Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His
 260 265 270
 Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro
 275 280 285
 Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile
 290 295 300
 Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu
 305 310 315 320
 Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile
 325 330 335
 Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr
 340 345 350
 Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu
 355 360 365
 Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu
 370 375 380
 Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr
 385 390 395 400
 Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His
 405 410 415
 Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln
 420 425 430

115 120 125 130 135 140 145 150 155 160 165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415 420 425 430

Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn
 435 440 445

Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 450 455 460

<210> 28
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 28
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Thr Lys Lys Thr Gln Leu
 20 25 30

Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
 35 40 45

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
 50 55 60

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
 65 70 75 80

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val
 85 90 95

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
 100 105 110

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
 115 120 125

Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp
 130 135 140

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
 145 150 155 160

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
 165 170 175

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg
 180 185 190

Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly
 195 200 205

Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln

210	215	220
Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr		
225	230	235 240
Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys		
	245	250 255
Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser		
	260	265 270
Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val		
	275	280 285
Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu		
	290	295 300
Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr		
	310	315 320
Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys		
	325	330 335
Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln		
	340	345 350
Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu		
	355	360 365
Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met		
	370	375 380
Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala		
	385	390 395 400
Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr		
	405	410 415
Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp		
	420	425 430
Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp		
	435	440 445
Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln		
	450	455 460
Pro Leu Ser Thr Pro Leu Ser His Ser Thr		
465	470	

<210> 29

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 29

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15
Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr
20 25 30
Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile
35 40 45
Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp
50 55 60
Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu
65 70 75 80
Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn
85 90 95
Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val
100 105 110
Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr
115 120 125
Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg
130 135 140
Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe
145 150 155 160
Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp
165 170 175
Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp
180 185 190
Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala
195 200 205
Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn
210 215 220
Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly
225 230 235 240
Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp
245 250 255
Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn
260 265 270
Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val
275 280 285
Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met
290 295 300
Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln

305 310 315 320
 Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro
 325 330 335

Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly
 340 345 350

Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn
 355 360 365

Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys
 370 375 380

Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly
 385 390 395 400

Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile
 405 410 415

Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu
 420 425 430

His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr
 435 440 445

Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro
 450 455 460

Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470

<210> 30

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
 construct of human CD39

<400> 30

Met Glu Thr Asp Thr Leu Leu Leu Trp Val Leu Leu Leu Trp Val Pro
 1 5 10 15

Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu
 20 25 30

Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
 35 40 45

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
 50 55 60

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
 65 70 75 80

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met

85

90

95

Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro
			100						105				110		
Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser
		115					120					125			
Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser
		130					135				140				
Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu
145					150					155					160
Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe
				165					170					175	
Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn
			180					185					190		
Gln	Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val
		195					200					205			
Thr	Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu
		210				215					220				
Gln	Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe
225					230					235					240
Leu	Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp
				245					250					255	
Ile	Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro
			260					265					270		
Gly	Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys
		275					280					285			
Thr	Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln
	290					295					300				
Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe
305					310					315					320
Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe
				325					330					335	
Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe
			340					345					350		
Val	Met	Lys	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys
		355					360					365			
Val	Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile
	370					375					380				
Lys	Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys
385					390					395					400
Phe	Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe

405

410

415

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
420 425 430

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met
435 440 445

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
450 455 460

<210> 31

<211> 58

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
50 55

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< 110 > Maliszewski, Charles R.
Gayle III, Richard B.
Marcus, Aaron J.
Immunex Corporation
Cornell Research Foundation, Inc.

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Recruitment

< 130 > 23,495 PCT

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< 150 > US 60/149,010

< 151 > 1999-08-13

< 160 > 31

< 170 > PatentIn Ver. 2.0

< 210 > 1

< 211 > 1599

< 212 > DNA

< 213 > Homo sapiens

< 220 >

< 221 > CDS

< 222 > (67)..(1596)

< 400 > 1

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ctactt atg gaa gat aca aag gag tct aac gtg aag aca ttt tgc tcc 108

Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser
1 5 10

aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata 156
Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
15 20 25 30

gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac 204
Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
35 40 45

gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta 252
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
50 55 60

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 300
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
65 70 75

cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt 348
His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
80 85 90

gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa 396
Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
95 100 105 110

aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt 444
Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
115 120 125

tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa 492
Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
130 135 140

gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac 540
Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
145 150 155

tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa 588
Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
160 165 170

ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt 636
 Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
 175 180 185 190

cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag 684
 Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
 195 200 205

gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act 732
 Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
 210 215 220

ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa 780
 Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
 225 230 235

ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg 828
 Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
 240 245 250

tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att 876
 Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
 255 260 265 270

cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga 924
 Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
 275 280 285

tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc 972
 Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
 290 295 300

aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt 1020
 Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
 305 310 315

att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac 1068
 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
 320 325 330

acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 1116
 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu

1116 1115 1114 1113 1112 1111 1110 1109 1108 1107 1106 1105 1104 1103 1102 1101 1100 1099 1098 1097 1096 1095 1094 1093 1092 1091 1090 1089 1088 1087 1086 1085 1084 1083 1082 1081 1080 1079 1078 1077 1076 1075 1074 1073 1072 1071 1070 1069 1068 1067 1066 1065 1064 1063 1062 1061 1060 1059 1058 1057 1056 1055 1054 1053 1052 1051 1050 1049 1048 1047 1046 1045 1044 1043 1042 1041 1040 1039 1038 1037 1036 1035 1034 1033 1032 1031 1030 1029 1028 1027 1026 1025 1024 1023 1022 1021 1020 1019 1018 1017 1016 1015 1014 1013 1012 1011 1010 1009 1008 1007 1006 1005 1004 1003 1002 1001 1000 999 998 997 996 995 994 993 992 991 990 989 988 987 986 985 984 983 982 981 980 979 978 977 976 975 974 973 972 971 970 969 968 967 966 965 964 963 962 961 960 959 958 957 956 955 954 953 952 951 950 949 948 947 946 945 944 943 942 941 940 939 938 937 936 935 934 933 932 931 930 929 928 927 926 925 924 923 922 921 920 919 918 917 916 915 914 913 912 911 910 909 908 907 906 905 904 903 902 901 900 899 898 897 896 895 894 893 892 891 890 889 888 887 886 885 884 883 882 881 880 879 878 877 876 875 874 873 872 871 870 869 868 867 866 865 864 863 862 861 860 859 858 857 856 855 854 853 852 851 850 849 848 847 846 845 844 843 842 841 840 839 838 837 836 835 834 833 832 831 830 829 828 827 826 825 824 823 822 821 820 819 818 817 816 815 814 813 812 811 810 809 808 807 806 805 804 803 802 801 800 799 798 797 796 795 794 793 792 791 790 789 788 787 786 785 784 783 782 781 780 779 778 777 776 775 774 773 772 771 770 769 768 767 766 765 764 763 762 761 760 759 758 757 756 755 754 753 752 751 750 749 748 747 746 745 744 743 742 741 740 739 738 737 736 735 734 733 732 731 730 729 728 727 726 725 724 723 722 721 720 719 718 717 716 715 714 713 712 711 710 709 708 707 706 705 704 703 702 701 700 699 698 697 696 695 694 693 692 691 690 689 688 687 686 685 684 683 682 681 680 679 678 677 676 675 674 673 672 671 670 669 668 667 666 665 664 663 662 661 660 659 658 657 656 655 654 653 652 651 650 649 648 647 646 645 644 643 642 641 640 639 638 637 636 635 634 633 632 631 630 629 628 627 626 625 624 623 622 621 620 619 618 617 616 615 614 613 612 611 610 609 608 607 606 605 604 603 602 601 600 599 598 597 596 595 594 593 592 591 590 589 588 587 586 585 584 583 582 581 580 579 578 577 576 575 574 573 572 571 570 569 568 567 566 565 564 563 562 561 560 559 558 557 556 555 554 553 552 551 550 549 548 547 546 545 544 543 542 541 540 539 538 537 536 535 534 533 532 531 530 529 528 527 526 525 524 523 522 521 520 519 518 517 516 515 514 513 512 511 510 509 508 507 506 505 504 503 502 501 500 499 498 497 496 495 494 493 492 491 490 489 488 487 486 485 484 483 482 481 480 479 478 477 476 475 474 473 472 471 470 469 468 467 466 465 464 463 462 461 460 459 458 457 456 455 454 453 452 451 450 449 448 447 446 445 444 443 442 441 440 439 438 437 436 435 434 433 432 431 430 429 428 427 426 425 424 423 422 421 420 419 418 417 416 415 414 413 412 411 410 409 408 407 406 405 404 403 402 401 400 399 398 397 396 395 394 393 392 391 390 389 388 387 386 385 384 383 382 381 380 379 378 377 376 375 374 373 372 371 370 369 368 367 366 365 364 363 362 361 360 359 358 357 356 355 354 353 352 351 350 349 348 347 346 345 344 343 342 341 340 339 338 337 336 335 334 333 332 331 330 329 328 327 326 325 324 323 322 321 320 319 318 317 316 315 314 313 312 311 310 309 308 307 306 305 304 303 302 301 300 299 298 297 296 295 294 293 292 291 290 289 288 287 286 285 284 283 282 281 280 279 278 277 276 275 274 273 272 271 270 269 268 267 266 265 264 263 262 261 260 259 258 257 256 255 254 253 252 251 250 249 248 247 246 245 244 243 242 241 240 239 238 237 236 235 234 233 232 231 230 229 228 227 226 225 224 223 222 221 220 219 218 217 216 215 214 213 212 211 210 209 208 207 206 205 204 203 202 201 200 199 198 197 196 195 194 193 192 191 190 189 188 187 186 185 184 183 182 181 180 179 178 177 176 175 174 173 172 171 170 169 168 167 166 165 164 163 162 161 160 159 158 157 156 155 154 153 152 151 150 149 148 147 146 145 144 143 142 141 140 139 138 137 136 135 134 133 132 131 130 129 128 127 126 125 124 123 122 121 120 119 118 117 116 115 114 113 112 111 110 109 108 107 106 105 104 103 102 101 100 99 98 97 96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1 0

335 340 345 350

cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg 1164
Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
355 360 365

atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1212
Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
370 375 380

act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1260
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
385 390 395

aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1308
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
400 405 410

tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1356
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Gln Gly Tyr His Phe Thr
415 420 425 430

gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1404
Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
435 440 445

gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1452
Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
450 455 460

cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc 1500
Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val
465 470 475

ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata 1548
Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile
480 485 490

ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta 1596
Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
495 500 505 510

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<210> 2

<211> 510

<212> PRT

<213> Homo sapiens

<400> 2

Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn
1 5 10 15

Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile Ala Leu
20 25 30

Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu
465 470 475 480

Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu
485 490 495

Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val
500 505 510

<210> 3

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 3

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile

50

55

60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145 150 155 160

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys

275

280

285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
 290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
 305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
 325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
 340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
 355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
 370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
 385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
 405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
 420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
 435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
 450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

<210> 4

<211> 476

<212> PRT

< 213 > Artificial Sequence

< 220 >

< 223 > Description of Artificial Sequence: Fusion
construct of human CD39

< 220 >

< 221 > VARIANT

< 222 > (39)

< 223 > Any amino acid, preferably Cys or Ser

< 400 > 4

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Met Xaa Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
50 55 60

Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
65 70 75 80

Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
85 90 95

Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
100 105 110

Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
115 120 125

Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
130 135 140

Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
145 150 155 160

165 170 175 180 185 190 195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380

Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala
165 170 175

Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
180 185 190

Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
195 200 205

Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
210 215 220

Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
225 230 235 240

Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
245 250 255

Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
260 265 270

Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
275 280 285

Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
290 295 300

Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
305 310 315 320

Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
325 330 335

Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro
340 345 350

Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys
355 360 365

Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu
370 375 380

Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser
385 390 395 400

Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly
405 410 415

Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp
420 425 430

Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala
435 440 445

Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala
450 455 460

Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470 475

<210> 5

<211> 1365

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<220>

<221> CDS

<222> (1)..(1362)

<400> 5

gca cct act tca agt tct aca aag aaa aca cag cta act agt tca acc 48

Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15

cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg gat 96

Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca gaa 144

Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
35 40 45

aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg gtt 192
Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
50 55 60

aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata ggc 240
Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly
65 70 75 80

att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca agg 288
Ile Tyr Leu Thr Asp Cys Met Gly Arg Ala Arg Glu Val Ile Pro Arg
85 90 95

tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc atg 336
Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
100 105 110

cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg gat 384
Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
115 120 125

gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt gcc 432
Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
130 135 140

agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act atc 480
Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
145 150 155 160

aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc ata 528
Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile
165 170 175

gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac ctt 576
Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu
180 185 190

ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act atc 624
Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile
195 200 205

gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac tac 672
 Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr
 210 215 220

aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca ctc 720
 Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu
 225 230 235 240

tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att ctc 768
 Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu
 245 250 255

agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta agt 816
 Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser
 260 265 270

gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt cca 864
 Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro
 275 280 285

ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc cat 912
 Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His
 290 295 300

caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc cag 960
 Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln
 305 310 315 320

tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt ggg 1008
 Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly
 325 330 335

gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca tca 1056
 Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser
 340 345 350

gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc tgt 1104
 Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
 355 360 365

gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag gag 1152
 Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu

370 375 380

aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc ctc 1200
Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
385 390 395 400

ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc cat 1248
Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
405 410 415

ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc tac 1296
Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr
420 425 430

atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc aca 1344
Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr
435 440 445

cct ctc tcc cac tcc acc taa 1365
Pro Leu Ser His Ser Thr
450

<210> 6
<211> 454
<212> PRT
<213> Artificial Sequence

<400> 6
Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu Thr Ser Ser Thr
1 5 10 15

Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu Asp
20 25 30

Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu
35 40 45

Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg Val
50 55 60

Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile Gly

65 70 75 80
Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro Arg
85 90 95
Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly Met
100 105 110
Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu Asp
115 120 125
Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala
130 135 140
Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile
145 150 155 160
Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile
165 170 175
Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu
180 185 190
Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr Ile
195 200 205
Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr
210 215 220
Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu
225 230 235 240
Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile Leu
245 250 255
Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val Ser
260 265 270
Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu Pro
275 280 285
Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His

290 295 300

Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln
305 310 315 320

Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly
325 330 335

Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser
340 345 350

Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys
355 360 365

Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu
370 375 380

Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu
385 390 395 400

Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile His
405 410 415

Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr
420 425 430

Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser Thr
435 440 445

Pro Leu Ser His Ser Thr
450

<210> 7

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
145 150 155 160

tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa 528
Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
165 170 175

ggt gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt 576
Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
180 185 190

cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag 624
Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln
195 200 205

gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act 672
Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
210 215 220

ttt gta ccc caa aac cag act atc gag tcc cca gat aat gct ctg caa 720
Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
225 230 235 240

ttt cgc ctc tat ggc aag gac tac aat gtc tac aca cat agc ttc ttg 768
Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
245 250 255

tgc tat ggg aag gat cag gca ctc tgg cag aaa ctg gcc aag gac att 816
Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
260 265 270

cag gtt gca agt aat gaa att ctc agg gac cca tgc ttt cat cct gga 864
Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
275 280 285

tat aag aag gta gtg aac gta agt gac ctt tac aag acc ccc tgc acc 912
Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
290 295 300

aag aga ttt gag atg act ctt cca ttc cag cag ttt gaa atc cag ggt 960
Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
305 310 315 320

att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac 1008
 Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
 325 330 335

acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg 1056
 Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
 340 345 350

cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg 1104
 Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
 355 360 365

atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg 1152
 Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
 370 375 380

act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa 1200
 Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
 385 390 395 400

aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt 1248
 Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
 405 410 415

tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca 1296
 Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr
 420 425 430

gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc 1344
 Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
 435 440 445

gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc 1392
 Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
 450 455 460

cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc taa 1437
 Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470 475

<210> 8

<211> 478

<212> PRT

<213> Artificial Sequence

<400> 8

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn
35 40 45

Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
50 55 60

Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
65 70 75 80

His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
85 90 95

Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
100 105 110

Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val
115 120 125

Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu
130 135 140

Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn
145 150 155 160

Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu
165 170 175

Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser
180 185 190

Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln

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195 200 205 210 215 220 225 230 235 240 245 250 255 260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400 405 410 415

195 200 205
Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr
210 215 220
Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln
225 230 235 240
Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu
245 250 255
Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile
260 265 270
Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly
275 280 285
Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr
290 295 300
Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly
305 310 315 320
Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn
325 330 335
Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu
340 345 350
Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val
355 360 365
Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val
370 375 380
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys
385 390 395 400
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe
405 410 415
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr

420 425 430

Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser
435 440 445

Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile
450 455 460

Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
465 470 475

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
signal sequence

<400> 9

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
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Ser Leu Ala Leu Val Thr Asn Ser
20

<210> 10

<211> 8

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
peptide

<400> 10

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

<210> 11
<211> 43
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 11
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
20 25 30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys
35 40

<210> 12
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 12
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys
20 25

<210> 13
<211> 31
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 13

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys
20 25 30

<210> 14

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 14

ccggctggac ttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60

tgtccacacc tctctcccac gagcccc

87

<210> 15

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 15

gacggggct cgtgggagag aggtgtggac aatggttgct cagctgggat catgttggtc 60

aggttcagca ttagcccaa agtccag

87

<210> 16
<211> 740
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (42)..(737)

<400> 16

cggtaccgct agcgtcgaca ggcctaggat atcgatacgt a gag ccc aga tct tgt 56

Glu Pro Arg Ser Cys

1 5

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggc 104

Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly

10 15 20

gcg ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 152

Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met

25 30 35

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 200

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His

40 45 50

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 248

Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val

55 60 65

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac 296

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr

70 75 80 85

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 344

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly

90 95 100

aag gac tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atg 392

Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Met

105 110 115

cag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg 440
 Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
 120 125 130

tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc agc 488
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser
 135 140 145

ctg acc tgc ctg gtc aaa ggc ttc tat ccc agg cac atc gcc gtg gag 536
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg His Ile Ala Val Glu
 150 155 160 165

tgg gag agc aat ggg cag ccg gag aac aac tac aag acc acg cct ccc 584
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
 170 175 180

gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg 632
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val
 185 190 195

gac aag agc agg tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg 680
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met
 200 205 210

cat gag gct ctg cac aac cac tac acg cag aag agc ctc tcc ctg tct 728
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
 215 220 225

ccg ggt aaa tga 740
 Pro Gly Lys
 230

<210> 17
 <211> 232
 <212> PRT
 <213> Homo sapiens

<400> 17
 Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
 1 5 10 15

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Pro Glu Ala Glu Gly Ala Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Met Gln Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Arg
145 150 155 160

His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 18
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 18
ctttccatcc tgagcaac 18

<210> 19
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 19
aaaaaactag tcagaacaaa gctttgccag aaaacg 36

<210> 20
<211> 24
<212> PRT
<213> Mus sp.

<400> 20

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser
20

<210> 21

<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 21
ctagttctgg agactacaaa gatgacgatg acaaaaccca gaacaa 46

<210> 22
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 22
agctttgttc tgggttttgc catcgatc tttgtagtct ccagaa 46

<210> 23
<211> 89
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 23
ccggctggac ttgggttac atgctgaacc tgaccaacat gatcccagct gagcaacat 60
tgtccacacc tctctccac tccacctaa 89

<210> 24
<211> 89

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
oligonucleotide

<400> 24
ggccttaggt ggagtgggag agaggtgtgg acaatggtg ctcagctggg atcatgttg 60
tcaggttcag catgtagccc aaagtccag 89

<210> 25
<211> 1464
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(1461)

<220>
<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 25
atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta 48
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
20 25 30

aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa 144
Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys
35 40 45

acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg 192
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
50 55 60

gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca 240
 Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
 65 70 75 80

gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg 288
 Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
 85 90 95

gtt aaa ggt cct gga atc tca aaa ttt gtt cag aaa gta aat gaa ata 336
 Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
 100 105 110

ggc att tac ctg act gat tgc atg gaa aga gct agg gaa gtg att cca 384
 Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
 115 120 125

agg tcc cag cac caa gag aca ccc gtt tac ctg gga gcc acg gca ggc 432
 Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
 130 135 140

atg cgg ttg ctc agg atg gaa agt gaa gag ttg gca gac agg gtt ctg 480
 Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
 145 150 155 160

gat gtg gtg gag agg agc ctc agc aac tac ccc ttt gac ttc cag ggt 528
 Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
 165 170 175

gcc agg atc att act ggc caa gag gaa ggt gcc tat ggc tgg att act 576
 Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
 180 185 190

atc aac tat ctg ctg ggc aaa ttc agt cag aaa aca agg tgg ttc agc 624
 Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
 195 200 205

ata gtc cca tat gaa acc aat aat cag gaa acc ttt gga gct ttg gac 672
 Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
 210 215 220

ctt ggg gga gcc tct aca caa gtc act ttt gta ccc caa aac cag act 720
 Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr

225 230 235 240

atc gag tcc cca gat aat gct ctg caa ttt cgc ctc tat ggc aag gac 768
Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp
245 250 255

tac aat gtc tac aca cat agc ttc ttg tgc tat ggg aag gat cag gca 816
Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
260 265 270

ctc tgg cag aaa ctg gcc aag gac att cag gtt gca agt aat gaa att 864
Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
275 280 285

ctc agg gac cca tgc ttt cat cct gga tat aag aag gta gtg aac gta 912
Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
290 295 300

agt gac ctt tac aag acc ccc tgc acc aag aga ttt gag atg act ctt 960
Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
305 310 315 320

cca ttc cag cag ttt gaa atc cag ggt att gga aac tat caa caa tgc 1008
Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
325 330 335

cat caa agc atc ctg gag ctc ttc aac acc agt tac tgc cct tac tcc 1056
His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser
340 345 350

cag tgt gcc ttc aat ggg att ttc ttg cca cca ctc cag ggg gat ttt 1104
Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe
355 360 365

ggg gca ttt tca gct ttt tac ttt gtg atg aag ttt tta aac ttg aca 1152
Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr
370 375 380

tca gag aaa gtc tct cag gaa aag gtg act gag atg atg aaa aag ttc 1200
Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe
385 390 395 400

tgt gct cag cct tgg gag gag ata aaa aca tct tac gct gga gta aag 1248
 Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys
 405 410 415

gag aag tac ctg agt gaa tac tgc ttt tct ggt acc tac att ctc tcc 1296
 Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser
 420 425 430

ctc ctt ctg caa ggc tat cat ttc aca gct gat tcc tgg gag cac atc 1344
 Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
 435 440 445

cat ttc att ggc aag atc cag ggc agc gac gcc ggc tgg act ttg ggc 1392
 His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
 450 455 460

tac atg ctg aac ctg acc aac atg atc cca gct gag caa cca ttg tcc 1440
 Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
 465 470 475 480

aca cct ctc tcc cac tcc acc taa 1464
 Thr Pro Leu Ser His Ser Thr
 485

<210> 26
 <211> 487
 <212> PRT
 <213> Artificial Sequence

<400> 26
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
 1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys
 20 25 30

Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys
 35 40 45

Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu
 50 55 60

1248 1296 1344 1392 1440 1464 1485 1500 1515 1530 1545 1560 1575 1590 1605 1620 1635 1650 1665 1680 1695 1710 1725 1740 1755 1770 1785 1800 1815 1830 1845 1860 1875 1890 1905 1920 1935 1950 1965 1980 1995 2010 2025 2040 2055 2070 2085 2100 2115 2130 2145 2160 2175 2190 2205 2220 2235 2250 2265 2280 2295 2310 2325 2340 2355 2370 2385 2400 2415 2430 2445 2460 2475 2490 2505 2520 2535 2550 2565 2580 2595 2610 2625 2640 2655 2670 2685 2700 2715 2730 2745 2760 2775 2790 2805 2820 2835 2850 2865 2880 2895 2910 2925 2940 2955 2970 2985 3000 3015 3030 3045 3060 3075 3090 3105 3120 3135 3150 3165 3180 3195 3210 3225 3240 3255 3270 3285 3300 3315 3330 3345 3360 3375 3390 3405 3420 3435 3450 3465 3480 3495 3510 3525 3540 3555 3570 3585 3600 3615 3630 3645 3660 3675 3690 3705 3720 3735 3750 3765 3780 3795 3810 3825 3840 3855 3870 3885 3900 3915 3930 3945 3960 3975 3990 4005 4020 4035 4050 4065 4080 4095 4110 4125 4140 4155 4170 4185 4200 4215 4230 4245 4260 4275 4290 4305 4320 4335 4350 4365 4380 4395 4410 4425 4440 4455 4470 4485 4500 4515 4530 4545 4560 4575 4590 4605 4620 4635 4650 4665 4680 4695 4710 4725 4740 4755 4770 4785 4800 4815 4830 4845 4860 4875 4890 4905 4920 4935 4950 4965 4980 4995 5010 5025 5040 5055 5070 5085 5100 5115 5130 5145 5160 5175 5190 5205 5220 5235 5250 5265 5280 5295 5310 5325 5340 5355 5370 5385 5400 5415 5430 5445 5460 5475 5490 5505 5520 5535 5550 5565 5580 5595 5610 5625 5640 5655 5670 5685 5700 5715 5730 5745 5760 5775 5790 5805 5820 5835 5850 5865 5880 5895 5910 5925 5940 5955 5970 5985 6000 6015 6030 6045 6060 6075 6090 6105 6120 6135 6150 6165 6180 6195 6210 6225 6240 6255 6270 6285 6300 6315 6330 6345 6360 6375 6390 6405 6420 6435 6450 6465 6480 6495 6510 6525 6540 6555 6570 6585 6600 6615 6630 6645 6660 6675 6690 6705 6720 6735 6750 6765 6780 6795 6810 6825 6840 6855 6870 6885 6900 6915 6930 6945 6960 6975 6990 7005 7020 7035 7050 7065 7080 7095 7110 7125 7140 7155 7170 7185 7200 7215 7230 7245 7260 7275 7290 7305 7320 7335 7350 7365 7380 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Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala
65 70 75 80

Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg
85 90 95

Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile
100 105 110

Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro
115 120 125

Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
130 135 140

Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu
145 150 155 160

Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly
165 170 175

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr
180 185 190

Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser
195 200 205

Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp
210 215 220

Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr
225 230 235 240

Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp
245 250 255

Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala
260 265 270

Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile
275 280 285

Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val
290 295 300

Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu
305 310 315 320

Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys
325 330 335

His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser
340 345 350

Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe
355 360 365

Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr
370 375 380

Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe
385 390 395 400

Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys
405 410 415

Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu Ser
420 425 430

Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu His Ile
435 440 445

His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr Leu Gly
450 455 460

Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro Leu Ser
465 470 475 480

Thr Pro Leu Ser His Ser Thr
485

<210> 27

<211> 464

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 27

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys Ala Leu Pro
20 25 30

Glu Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr
35 40 45

Ser Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly
50 55 60

Val Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser
65 70 75 80

Lys Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys
85 90 95

Met Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr
100 105 110

Pro Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu
115 120 125

Ser Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu
130 135 140

Ser Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln
145 150 155 160

Glu Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys
165 170 175

Phe Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn
180 185 190

Asn Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln
195 200 205

Val Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala
210 215 220

Leu Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser
225 230 235 240

Phe Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys
245 250 255

Asp Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His
260 265 270

Pro Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro
275 280 285

Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile
290 295 300

Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu
305 310 315 320

Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile
325 330 335

Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr
340 345 350

Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu
355 360 365

Lys Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu
370 375 380

Ile Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr
385 390 395 400

Cys Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His
405 410 415

Phe Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln
420 425 430

Gly Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn
435 440 445

Met Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
450 455 460

<210> 28

<211> 474

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 28

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Thr Lys Lys Thr Gln Leu
20 25 30

Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly
35 40 45

Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys
50 55 60

Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu
65 70 75 80

Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val

85 90 95

Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu
100 105 110

Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala
115 120 125

Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp
130 135 140

Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp
145 150 155 160

Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly
165 170 175

Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg
180 185 190

Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly
195 200 205

Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln
210 215 220

Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr
225 230 235 240

Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys
245 250 255

Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser
260 265 270

Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val
275 280 285

Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu
290 295 300

Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr

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305 310 315 320
 Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys
 325 330 335
 Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln
 340 345 350
 Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu
 355 360 365
 Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met
 370 375 380
 Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala
 385 390 395 400
 Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr
 405 410 415
 Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp
 420 425 430
 Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp
 435 440 445
 Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln
 450 455 460
 Pro Leu Ser Thr Pro Leu Ser His Ser Thr
 465 470

<210> 29
 <211> 473
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Fusion
 construct of human CD39

姓名	性别	年龄	职业	住址	联系电话	电子邮箱	身份证号	银行卡号	支付宝账号	微信账号	QQ账号	其他联系方式
张三	男	35	教师	北京市海淀区中关村大街100号	13800138000	zhangsan@163.com	110101198801010001	62284801010101010101	15171717171	zhangsan123	123456789	无
李四	女	28	程序员	北京市朝阳区望京SOHO	15001010101	lisi@126.com	110105199005050002	62284801010101010101	15171717171	lisi456	987654321	无
王五	男	42	医生	上海市浦东新区世纪大道100号	13900139000	wangwu@126.com	310101197801010001	62284801010101010101	15171717171	wangwu789	112233445	无
赵六	女	30	设计师	广东省深圳市福田区华强北路100号	13700137000	zhaoliu@126.com	440101198801010001	62284801010101010101	15171717171	zhaoliu123	556677889	无
孙七	男	38	工程师	浙江省杭州市西湖区文三路100号	13600136000	sunqi@126.com	330101197801010001	62284801010101010101	15171717171	sunqi456	223344556	无
周八	女	25	销售	江苏省南京市鼓楼区中山路100号	13500135000	zhouba@126.com	320101199001010001	62284801010101010101	15171717171	zhouba789	334455667	无
吴九	男	40	律师	北京市西城区金融大街100号	13900139000	wujiu@126.com	110101197801010001	62284801010101010101	15171717171	wujiu123	445566778	无
郑十	女	32	会计	山东省济南市经二路100号	13800138000	zhengshi@126.com	370101198801010001	62284801010101010101	15171717171	zhengshi456	556677889	无
冯十一	男	36	经理	河南省郑州市郑东新区CBD	13700137000	fengshi1@126.com	410101197801010001	62284801010101010101	15171717171	fengshi1789	667788990	无
陈十二	女	29	教师	四川省成都市高新区天府大道100号	13600136000	chenshi2@126.com	510101199001010001	62284801010101010101	15171717171	chenshi2123	778899001	无
林十三	男	41	医生	广东省广州市天河区珠江新城100号	13900139000	linshi3@126.com	440101197801010001	62284801010101010101	15171717171	linshi3456	889900112	无
周十四	女	33	程序员	浙江省杭州市余杭区未来科技城100号	13800138000	zhoushi4@126.com	330101198801010001	62284801010101010101	15171717171	zhoushi4789	990011223	无
吴十五	男	39	工程师	江苏省南京市江宁区江宁街道100号	13700137000	wushi5@126.com	320101197801010001	62284801010101010101	15171717171	wushi5123	001122334	无
郑十六	女	27	销售	北京市丰台区丽泽商务区100号	13600136000	zhengshi6@126.com	110101199001010001	62284801010101010101	15171717171	zhengshi6456	112233445	无
冯十七	男	43	律师	山东省济南市经二路100号	13900139000	fengshi7@126.com	370101197801010001	62284801010101010101	15171717171	fengshi7789	223344556	无
陈十八	女	31	会计	河南省郑州市郑东新区CBD	13800138000	chenshi8@126.com	410101198801010001	62284801010101010101	15171717171	chenshi8123	334455667	无
林十九	男	37	经理	四川省成都市高新区天府大道100号	13700137000	linshi9@126.com	510101197801010001	62284801010101010101	15171717171	linshi9456	445566778	无
周二十	女	26	教师	广东省广州市天河区珠江新城100号	13600136000	zhoushi0@126.com	440101199001010001	62284801010101010101	15171717171	zhoushi0789	556677889	无

Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr
20 25 30

Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp
50 55 60

Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn
85 90 95

Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr
115 120 125

Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe
145 150 155 160

Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp
165 170 175

Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp
180 185 190

Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala
195 200 205

Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn

His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp Thr
435 440 445

Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln Pro
450 455 460

Leu Ser Thr Pro Leu Ser His Ser Thr
465 470

<210> 30

<211> 463

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion
construct of human CD39

<400> 30

Met Glu Thr Asp Thr Leu Leu Trp Val Leu Leu Leu Trp Val Pro
1 5 10 15

Gly Ser Thr Gly Ala Pro Thr Ser Thr Gln Asn Lys Ala Leu Pro Glu
20 25 30

Asn Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser
35 40 45

Leu Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val
50 55 60

Val His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys
65 70 75 80

Phe Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met
85 90 95

Glu Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro
100 105 110

Val Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser

115 120 125
 Glu Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser
 130 135 140
 Asn Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu
 145 150 155 160
 Glu Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe
 165 170 175
 Ser Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn
 180 185 190
 Gln Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val
 195 200 205
 Thr Phe Val Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu
 210 215 220
 Gln Phe Arg Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe
 225 230 235 240
 Leu Cys Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp
 245 250 255
 Ile Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro
 260 265 270
 Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys
 275 280 285
 Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln
 290 295 300
 Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe
 305 310 315 320
 Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe
 325 330 335
 Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe

340 345 350

Val Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys
355 360 365

Val Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile
370 375 380

Lys Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys
385 390 395 400

Phe Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe
405 410 415

Thr Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly
420 425 430

Ser Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met
435 440 445

Ile Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr
450 455 460

<210> 31

<211> 58

<212> PRT

<213> Homo sapiens

<400> 31

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
1 5 10 15

Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
20 25 30

Ile Phe Leu Ser Ser Met Cys Pro Ile Asn Val Ser Ala Ser Thr Leu
35 40 45

Tyr Gly Ile Met Phe Asp Ala Gly Ser Thr
50 55